SEQUENCE LISTING

<110> Cardio, Inc.

5   <120> three dimensional tissue contruct

<130> CD009PCT

<150> JP2003-285476
10 <151> 2003-08-01

<160> 20

<170> PatentIn version 3.1
15
<210> 1
<211> 5956
<212> DNA
<213> Homo sapiens
20
<400> 1

```
atgagttctg actcagaatt ggctgttttt ggggaggctg ctcctttcct ccgaaagtct     60

gaaagggaac gcattgaggc ccagaatagg ccctttgatg ccaaaacatc tgtctttgtg    120

gcggagccca aagaatcctt tgtcaaaggg accatccaga gcagagaagg aggaaaagtg    180

acggtgaaga ctgagggagg agcgactctg acagtgaagg atgatcaggt cttccccatg    240

aaccctccca aatatgacaa gatcgaggat atggccatga tgactcatct gcatgagcct    300

gctgtgctgt acaacctcaa agaacgttat gcagcctgga tgatctacac ctattcaggt    360

ctcttctgtg tcactgtcaa cccctacaag tggctgcctg tgtataagcc cgaggtggtg    420

acagcctacc gaggcaaaaa gcgccaggag gccccgcccc acatcttctc catctctgac    480

aacgcctatc agttcatgct gactgaccga gagaatcagt caatcctgat cactggagaa    540

tctggtgcag ggaagactgt gaacaccaag cgtgtcatcc agtactttgc aacaattgca    600

gttactggtg agaagaagaa ggaagaaatt acttctggca aaatacaggg gactctggaa    660

gatcaaatca tcagtgccaa cccctactg gaggcctttg gcaacgccaa gaccgtgagg    720

aatgacaact cctctcgctt tggtaaattc atcagaatcc actttggcac tactggaaaa    780

ctggcatctg ctgatattga aacatatctg ctagagaagt ctagagttgt tttccagctt    840
```

```
     aaggctgaga gaagttatca tattttttac cagattacat cgaataagaa accagaactt   900

     attgaaatgc ttctgattac cacgaaccca tatgattacc catttgtcag tcaaggggag   960
5
     atcagtgtgg ccagcatcga tgatcaggaa gaactgatgg ccacagatag tgctattgat   1020

     attttgggct ttactaatga agaaaaggtc tccatttaca agctcacggg ggctgtgatg   1080
10
     cattatggga acctaaaatt taagcaaaag cagcgtgagg agcaagcaga gccagatggc   1140

     acagaagttg ctgacaaggc ggcctacctc cagagtctga actctgcaga tctgctcaaa   1200
15
     gctctctgct accccagggt caaggtcggc aatgagtatg tcaccaaagg ccagactgta   1260

     gaacaggtgt ccaacgcagt aggtgctctg gccaaagccg tctacgagaa gatgttcctg   1320

     tggatggttg cccgcatcaa ccagcagctg gacaccaagc agcccaggca gtacttcatc   1380
20
     ggggtcttgg acattgctgg ttttgagatt tttgatttca acagcctgga gcagctgtgc   1440

     atcaatttca ccaatgagaa actgcaacag ttttttcaacc accacatgtt cgtgctggag   1500
25
     caggaggagt acaagaagga aggcatcgag tggacgttca tcgacttcgg gatggacctg   1560

     gctgcctgca tcgagctcat cgagaagcct atgggcatct tctccatcct ggaagaggag   1620

     tgcatgttcc ctaaggcaac agacacctcc ttcaagaaca agctgtatga ccagcacctg   1680
30
     ggcaagtctg ccaacttcca gaagcccaag gtggtcaaag gcaaggccga ggcccacttc   1740

     gctctgattc actatgctgg tgttgtggac tacaacatta ctggctggct ggagaagaac   1800
35
     aaggaccccc tgaatgagac cgtggttgga ctgtaccaga agtctgcaat gaaaactcta   1860

     gctcagctct tctctggggc tcaaactgct gaaggagagg gagctggtgg aggggccaag   1920

     aaaggtggta agaagaaggg ctcttctttc cagacagtgt ctgccctttt cagagagaat   1980
40
     ttgaacaagc tgatgaccaa cctcaggagt acccatcctc actttgtgag gtgtatcatc   2040

     cccaatgaga caaaaactcc tggtgccatg gagcatgagc ttgtcctcca ccagctgagg   2100

     tgtaacggtg tgctggaagg catccgcatc tgtaggaaag gatttccaag cagaatcctt   2160
45
     tatgcagact tcaaacagag atacaaggta ttaaatgcaa gtgcaatccc tgaagggcaa   2220

     ttcattgata gcaagaaggc ctctgagaag ctccttgcat ccatcgacat tgaccacacc.   2280
```

```
        cagtataaat ttgggcacac caaggtcttt ttcaaagctg gtcttctggg gctcctagag   2340

        gagatgcgag atgacaagct ggcccagctg attacccgaa cccaggccag gtgcagaggg   2400
   5
        ttcttggcaa gagtggagta ccagaggatg gtggagagaa gggaggccat cttctgtatc   2460

        cagtacaata tcagatcctt catgaatgtc aagcactggc cctggatgaa actcttcttc   2520

  10    aagatcaagc ctctgttgaa gagtgcagaa actgagaagg agatggccac catgaaggaa   2580

        gaatttcaga aaattaaaga cgaacttgcc aagtcagagg caaaaaggaa ggaactggaa   2640

        gaaaagatgg tgacgctgtt gaaagaaaaa aatgacttgc agctccaagt tcaggctgaa   2700
  15
        gccgaaggct tggctgatgc agaggaaagg tgtgaccagc taatcaaaac caaaatccag   2760

        ctagaagcca aaatcaaaga ggtgactgag agagctgagg atgaggaaga gatcaatgct   2820

  20    gagctgacag ccaagaagag gaaactggag gatgaatgtt cagaactcaa gaaagacatt   2880

        gatgaccttg agctgacact ggccaaggtt gagaaggaga aacatgccac agaaaacaag   2940

        gtgaaaaacc tcacagaaga gatggcaggt ctggatgaaa ccattgctaa gctgaccaag   3000
  25
        gagaagaagg ctctccagga ggcccaccag cagaccctgg atgacctgca ggcagaggag   3060

        gacaaagtca acaccctgac caaagctaaa atcaaacttg aacaacaagt ggatgatctt   3120

  30    gaagggtcct tggagcaaga aaagaaactt cgcatggacc tagaaagggc taagaggaaa   3180

        cttgagggtg acttgaagtt ggcccaagaa tccataatgg acattgaaaa tgagaaacag   3240

        caacttgatg aaaagctcaa aaagaaagag tttgaaatca gcaatctgca aagcaagatt   3300
  35
        gaagatgaac aggcacttgg cattcaattg cagaagaaaa ttaaagaatt gcaagcccgc   3360

        attgaggagc tggaggagga aatcgaggcg gagcgggcct cccgggccaa agcagagaag   3420

  40    cagcgctctg acctctcccg ggagctggag gagatcagcg agaggctgga agaagccggt   3480

        ggggccactt cagcccagat tgagatgaac aagaagcggg aggctgagtt ccagaaaatg   3540

        cgcagggacc tggaggaggc caccctacag catgaagcca cagcggccac cctgaggaag   3600
  45
        aagcatgcag atagtgtggc cgagcttggg gagcagattg acaacctgca gcgagtgaag   3660

        cagaagctgg agaaggagaa gagtgagatg aagatggaga ttgatgacct tgctagtaat   3720
```

```
gtagaaacgg tctccaaagc caagggaaac ctagagaaaa tgtgccggac tctagaggac   3780

caactgagtg aactgaaatc aaaggaagag gagcagcagc ggctgatcaa tgacctgact   3840

gcgcagaggg ggcgcctgca gactgaatct ggtgagtttt cacgccagct tgatgaaaag   3900

gaagctctgg tgtctcagtt atcaagaggc aaacaagcct ttactcaaca gattgaagaa   3960

ttaaagaggc aacttgaaga ggagataaaa gccaagaacg ccctggcgca tgccctgcag   4020

tcttcccgcc acgactgtga cctgctgcgg gaacagtatg aggaggagca ggaatccaag   4080

gccgagctgc agagagcact gtccaaggcc aacaccgagg ttgcccaatg gaggaccaaa   4140

tacgagacgg acgccatcca gcgcacagag gagctggagg aggccaagaa gaagctggcc   4200

cagcggctgc aggcagctga ggaacatgta gaagctgtga acgccaaatg tgcttccctc   4260

gaaaagacga agcagcggct gcagaatgag gtcgaggacc tcatgcttga tgtggagagg   4320

acaaatgccg cctgtgccgc ccttgacaaa aagcaaagga acttcgataa gatcctggca   4380

gaatggaaac agaaatgtga ggaaacgcat gctgagcttg aggcctccca gaaggaggcc   4440

cgttcccttg gcactgagct gttcaagata aagaatgcct atgaggaatc tttggatcag   4500

ctagaaaccc tgaagcgaga gaacaaaaac ttacagcagg agatttctga cctcacggaa   4560

cagattgcag aaggagggaa acgtatccat gaactggaga aaataaagaa acaagtggaa   4620

caagaaaagt gtgaacttca ggctgcttta gaagaagcag aggcatctct tgaacatgaa   4680

gagggaaaga tcctgcgcat ccagcttgag ttgaaccaag tcaagtctga ggttgatagg   4740

aaaattgctg aaaaagatga ggaaattgac cagctgaaga gaaaccacat tagaatcgtg   4800

gagtccatgc agagcacgct ggatgctgag atcaggagta ggaatgatgc cattaggctc  ·4860

aagaagaaga tggagggaga cctcaatgaa atggaaatcc agctgaacca tgccaaccgc   4920

atggctgctg aggccctgag gaactacagg aacacccaag gcatcctcaa ggatacccag   4980

atccacctgg atgatgctct ccggagccag gaggacctga aggaacagct ggccatggtg   5040

gagcgcagag ccaacctgct gcaggctgag atcgaggagc tgcgggccac tctggaacag   5100

acagagagga gcagaaaaat cgcagaacag gagctcctgg atgccagtga gcgtgttcag   5160
```

```
        ctactgcaca cccagaacac cagcctgatc aacaccaaga agaagctgga gacagatatt   5220

        tcccaaatgc aaggagagat ggaggacatt ctccaggaag cccgcaatgc agaagaaaag   5280
   5
        gccaagaagg ccatcactga tgccgccatg atggctgagg agctgaagaa ggagcaggac   5340

        accagcgccc acctggagcg gatgaagaag aacatggagc agaccgtgaa ggatctgcag   5400

  10    ctccgtctgg atgaggctga gcagctggcc ctgaagggtg ggaagaagca gatccagaaa   5460

        ctggaggcca gggtacggga gctggaagga gaggttgaga gtgagcaaaa gcgtaatgct   5520

        gaggctgtca aaggtctgcg caaacatgag aggcgagtga aggaactcac ttaccagacg   5580
  15
        gaagaagata gaaagaatat tctcaggctt caagatttgg tagataaact tcaggcaaaa   5640

        gtgaaatctt ataagagaca agctgaggag gctgaggaac aatccaacac caatctagct   5700

  20    aaattccgca agctccagca tgagctggag gaggccgagg aacgggctga cattgctgag   5760

        tcccaggtga acaaactgcg ggtgaagagc cgggaggttc acacaaaagt cataagtgaa   5820

        gagtgatcat gtcctgatgc catggaatga ctgaagacag gcacaaaatg tgacatcttt   5880
  25
        ggtcatttcc ctctgtaatt attgtgtatt ctaccctgtt gcaaaggaaa taaagcatag   5940

        ggtagtttgc aaacaa                                                    5956
```

```
  30
        <210>  2
        <211>  1941
        <212>  PRT
        <213>  Homo sapiens
  35
        <400>  2

        Met Ser Ser Asp Ser Glu Leu Ala Val Phe Gly Glu Ala Ala Pro Phe
        1               5                   10                  15
  40

        Leu Arg Lys Ser Glu Arg Glu Arg Ile Glu Ala Gln Asn Arg Pro Phe
                        20                  25                  30

  45
        Asp Ala Lys Thr Ser Val Phe Val Ala Glu Pro Lys Glu Ser Phe Val
                        35                  40                  45
```

Lys Gly Thr Ile Gln Ser Arg Glu Gly Gly Lys Val Thr Val Lys Thr
    50   55   60

5

Glu Gly Gly Ala Thr Leu Thr Val Lys Asp Asp Gln Val Phe Pro Met
    65   70   75   80

10 Asn Pro Pro Lys Tyr Asp Lys Ile Glu Asp Met Ala Met Met Thr His
                85   90   95

Leu His Glu Pro Ala Val Leu Tyr Asn Leu Lys Glu Arg Tyr Ala Ala
15   100   105   110

Trp Met Ile Tyr Thr Tyr Ser Gly Leu Phe Cys Val Thr Val Asn Pro
        115   120   125
20

Tyr Lys Trp Leu Pro Val Tyr Lys Pro Glu Val Val Thr Ala Tyr Arg
    130   135   140

25

Gly Lys Lys Arg Gln Glu Ala Pro Pro His Ile Phe Ser Ile Ser Asp
145   150   155   160

30 Asn Ala Tyr Gln Phe Met Leu Thr Asp Arg Glu Asn Gln Ser Ile Leu
            165   170   175

Ile Thr Gly Glu Ser Gly Ala Gly Lys Thr Val Asn Thr Lys Arg Val
35   180   185   190

Ile Gln Tyr Phe Ala Thr Ile Ala Val Thr Gly Glu Lys Lys Lys Glu
    195   200   205
40

Glu Ile Thr Ser Gly Lys Ile Gln Gly Thr Leu Glu Asp Gln Ile Ile
    210   215   220

45

Ser Ala Asn Pro Leu Leu Glu Ala Phe Gly Asn Ala Lys Thr Val Arg
225   230   235   240

Asn Asp Asn Ser Ser Arg Phe Gly Lys Phe Ile Arg Ile His Phe Gly
                 245   250   255

5

Thr Thr Gly Lys Leu Ala Ser Ala Asp Ile Glu Thr Tyr Leu Leu Glu
         260   265   270

10   Lys Ser Arg Val Val Phe Gln Leu Lys Ala Glu Arg Ser Tyr His Ile
           275   280   285

Phe Tyr Gln Ile Thr Ser Asn Lys Lys Pro Glu Leu Ile Glu Met Leu
15   290   295   300

Leu Ile Thr Thr Asn Pro Tyr Asp Tyr Pro Phe Val Ser Gln Gly Glu
305   310   315   320
20

Ile Ser Val Ala Ser Ile Asp Asp Gln Glu Glu Leu Met Ala Thr Asp
         325   330   335

25

Ser Ala Ile Asp Ile Leu Gly Phe Thr Asn Glu Glu Lys Val Ser Ile
        340   345   350

30   Tyr Lys Leu Thr Gly Ala Val Met His Tyr Gly Asn Leu Lys Phe Lys
         355   360   365

Gln Lys Gln Arg Glu Glu Gln Ala Glu Pro Asp Gly Thr Glu Val Ala
35   370   375   380

Asp Lys Ala Ala Tyr Leu Gln Ser Leu Asn Ser Ala Asp Leu Leu Lys
385   390   395   400
40

Ala Leu Cys Tyr Pro Arg Val Lys Val Gly Asn Glu Tyr Val Thr Lys
        405   410   415

45

Gly Gln Thr Val Glu Gln Val Ser Asn Ala Val Gly Ala Leu Ala Lys
        420   425   430

Ala Val Tyr Glu Lys Met Phe Leu Trp Met Val Ala Arg Ile Asn Gln
    435   440   445

5

Gln Leu Asp Thr Lys Gln Pro Arg Gln Tyr Phe Ile Gly Val Leu Asp
    450   455   460

10   Ile Ala Gly Phe Glu Ile Phe Asp Phe Asn Ser Leu Glu Gln Leu Cys
    465   470   475   480

Ile Asn Phe Thr Asn Glu Lys Leu Gln Gln Phe Phe Asn His His Met
15   485   490   495

Phe Val Leu Glu Gln Glu Glu Tyr Lys Lys Glu Gly Ile Glu Trp Thr
        500   505   510
20

Phe Ile Asp Phe Gly Met Asp Leu Ala Ala Cys Ile Glu Leu Ile Glu
      515   520   525

25

Lys Pro Met Gly Ile Phe Ser Ile Leu Glu Glu Glu Cys Met Phe Pro
    530   535   540

30   Lys Ala Thr Asp Thr Ser Phe Lys Asn Lys Leu Tyr Asp Gln His Leu
    545   550   555   560

Gly Lys Ser Ala Asn Phe Gln Lys Pro Lys Val Val Lys Gly Lys Ala
35   565   570   575

Glu Ala His Phe Ala Leu Ile His Tyr Ala Gly Val Val Asp Tyr Asn
      580   585   590
40

Ile Thr Gly Trp Leu Glu Lys Asn Lys Asp Pro Leu Asn Glu Thr Val
      595   600   605

45

Val Gly Leu Tyr Gln Lys Ser Ala Met Lys Thr Leu Ala Gln Leu Phe
    610   615   620

```
        Ser Gly Ala Gln Thr Ala Glu Gly Glu Gly Ala Gly Gly Gly Ala Lys
        625               630             635             640

5

        Lys Gly Gly Lys Lys Lys Gly Ser Ser Phe Gln Thr Val Ser Ala Leu
                      645             650             655

10      Phe Arg Glu Asn Leu Asn Lys Leu Met Thr Asn Leu Arg Ser Thr His
                      660             665             670

        Pro His Phe Val Arg Cys Ile Ile Pro Asn Glu Thr Lys Thr Pro Gly
15              675             680             685

        Ala Met Glu His Glu Leu Val Leu His Gln Leu Arg Cys Asn Gly Val
            690             695             700
20

        Leu Glu Gly Ile Arg Ile Cys Arg Lys Gly Phe Pro Ser Arg Ile Leu
        705             710             715             720

25

        Tyr Ala Asp Phe Lys Gln Arg Tyr Lys Val Leu Asn Ala Ser Ala Ile
                      725             730             735

30      Pro Glu Gly Gln Phe Ile Asp Ser Lys Lys Ala Ser Glu Lys Leu Leu
                      740             745             750

        Ala Ser Ile Asp Ile Asp His Thr Gln Tyr Lys Phe Gly His Thr Lys
35              755             760             765

        Val Phe Phe Lys Ala Gly Leu Leu Gly Leu Leu Glu Glu Met Arg Asp
            770             775             780
40

        Asp Lys Leu Ala Gln Leu Ile Thr Arg Thr Gln Ala Arg Cys Arg Gly
        785             790             795             800

45

        Phe Leu Ala Arg Val Glu Tyr Gln Arg Met Val Glu Arg Arg Glu Ala
                      805             810             815
```

Ile Phe Cys Ile Gln Tyr Asn Ile Arg Ser Phe Met Asn Val Lys His
        820   825   830

5

Trp Pro Trp Met Lys Leu Phe Phe Lys Ile Lys Pro Leu Leu Lys Ser
      835   840   845

10 Ala Glu Thr Glu Lys Glu Met Ala Thr Met Lys Glu Glu Phe Gln Lys
     850   855   860

Ile Lys Asp Glu Leu Ala Lys Ser Glu Ala Lys Arg Lys Glu Leu Glu
15 865   870   875   880

Glu Lys Met Val Thr Leu Leu Lys Glu Lys Asn Asp Leu Gln Leu Gln
        885   890   895

20

Val Gln Ala Glu Ala Glu Gly Leu Ala Asp Ala Glu Glu Arg Cys Asp
        900   905   910

25

Gln Leu Ile Lys Thr Lys Ile Gln Leu Glu Ala Lys Ile Lys Glu Val
      915   920   925

30 Thr Glu Arg Ala Glu Asp Glu Glu Glu Ile Asn Ala Glu Leu Thr Ala
     930   935   940

Lys Lys Arg Lys Leu Glu Asp Glu Cys Ser Glu Leu Lys Lys Asp Ile
35 945   950   955   960

Asp Asp Leu Glu Leu Thr Leu Ala Lys Val Glu Lys Glu Lys His Ala
        965   970   975

40

Thr Glu Asn Lys Val Lys Asn Leu Thr Glu Glu Met Ala Gly Leu Asp
        980   985   990

45

Glu Thr Ile Ala Lys Leu Thr Lys Glu Lys Lys Ala Leu Gln Glu Ala
      995   1000   1005

His Gln Gln Thr Leu Asp Asp Leu Gln Ala Glu Glu Asp Lys Val
    1010   1015   1020

5

Asn Thr Leu Thr Lys Ala Lys Ile Lys Leu Glu Gln Gln Val Asp
    1025   1030   1035

10 Asp Leu Glu Gly Ser Leu Glu Gln Glu Lys Lys Leu Arg Met Asp
        1040   1045   1050

Leu Glu Arg Ala Lys Arg Lys Leu Glu Gly Asp Leu Lys Leu Ala
15   1055   1060   1065

Gln Glu Ser Ile Met Asp Ile Glu Asn Glu Lys Gln Gln Leu Asp
    1070   1075   1080
20

Glu Lys Leu Lys Lys Lys Glu Phe Glu Ile Ser Asn Leu Gln Ser
    1085   1090   1095

25

Lys Ile Glu Asp Glu Gln Ala Leu Gly Ile Gln Leu Gln Lys Lys
    1100   1105   1110

30 Ile Lys Glu Leu Gln Ala Arg Ile Glu Glu Leu Glu Glu Glu Ile
        1115   1120   1125

Glu Ala Glu Arg Ala Ser Arg Ala Lys Ala Glu Lys Gln Arg Ser
35   1130   1135   1140

Asp Leu Ser Arg Glu Leu Glu Glu Ile Ser Glu Arg Leu Glu Glu
    1145   1150   1155
40

Ala Gly Gly Ala Thr Ser Ala Gln Ile Glu Met Asn Lys Lys Arg
    1160   1165   1170

45

Glu Ala Glu Phe Gln Lys Met Arg Arg Asp Leu Glu Glu Ala Thr
    1175   1180   1185

Leu Gln His Glu Ala Thr Ala Ala Thr Leu Arg Lys Lys His Ala
    1190   1195   1200

5

Asp Ser Val Ala Glu Leu Gly Glu Gln Ile Asp Asn Leu Gln Arg
    1205   1210   1215

10 Val Lys Gln Lys Leu Glu Lys Glu Lys Ser Glu Met Lys Met Glu
    1220   1225   1230

Ile Asp Asp Leu Ala Ser Asn Val Glu Thr Val Ser Lys Ala Lys
15   1235   1240   1245

Gly Asn Leu Glu Lys Met Cys Arg Thr Leu Glu Asp Gln Leu Ser
    1250   1255   1260
20

Glu Leu Lys Ser Lys Glu Glu Glu Gln Gln Arg Leu Ile Asn Asp
    1265   1270   1275

25

Leu Thr Ala Gln Arg Gly Arg Leu Gln Thr Glu Ser Gly Glu Phe
    1280   1285   1290

30 Ser Arg Gln Leu Asp Glu Lys Glu Ala Leu Val Ser Gln Leu Ser
    1295   1300   1305

Arg Gly Lys Gln Ala Phe Thr Gln Gln Ile Glu Glu Leu Lys Arg
35   1310   1315   1320

Gln Leu Glu Glu Glu Ile Lys Ala Lys Asn Ala Leu Ala His Ala
    1325   1330   1335
40

Leu Gln Ser Ser Arg His Asp Cys Asp Leu Leu Arg Glu Gln Tyr
    1340   1345   1350

45

Glu Glu Glu Gln Glu Ser Lys Ala Glu Leu Gln Arg Ala Leu Ser
    1355   1360   1365

Lys Ala Asn Thr Glu Val Ala Gln Trp Arg Thr Lys Tyr Glu Thr
    1370   1375   1380

5

Asp Ala Ile Gln Arg Thr Glu Glu Leu Glu Glu Ala Lys Lys Lys
    1385   1390   1395 .

10 Leu Ala Gln Arg Leu Gln Ala Ala Glu Glu His Val Glu Ala Val
        1400   1405   1410

Asn Ala Lys Cys Ala Ser Leu Glu Lys Thr Lys Gln Arg Leu Gln
15   1415   1420   1425

Asn Glu Val Glu Asp Leu Met Leu Asp Val Glu Arg Thr Asn Ala
    1430   1435   1440
20

Ala Cys Ala Ala Leu Asp Lys Lys Gln Arg Asn Phe Asp Lys Ile
    1445   1450   1455

25

Leu Ala Glu Trp Lys Gln Lys Cys Glu Glu Thr His Ala Glu Leu
    1460   1465   1470

30 Glu Ala Ser Gln Lys Glu Ala Arg Ser Leu Gly Thr Glu Leu Phe
        1475   1480   1485

Lys Ile Lys Asn Ala Tyr Glu Glu Ser Leu Asp Gln Leu Glu Thr
35   1490   1495   1500

Leu Lys Arg Glu Asn Lys Asn Leu Gln Gln Glu Ile Ser Asp Leu
    1505   1510   1515
40

Thr Glu Gln Ile Ala Glu Gly Gly Lys Arg Ile His Glu Leu Glu
    1520   1525   · 1530

45

Lys Ile Lys Lys Gln Val Glu Gln Glu Lys Cys Glu Leu Gln Ala
    1535   1540   1545

Ala Leu Glu Glu Ala Glu Ala Ser Leu Glu His Glu Glu Gly Lys
    1550   1555   1560

5

Ile Leu Arg Ile Gln Leu Glu Leu Asn Gln Val Lys Ser Glu Val
    1565   1570   1575

10   Asp Arg Lys Ile Ala Glu Lys Asp Glu Glu Ile Asp Gln Leu Lys
         1580   1585   1590

Arg Asn His Ile Arg Ile Val Glu Ser Met Gln Ser Thr Leu Asp
15   1595   1600   1605

Ala Glu Ile Arg Ser Arg Asn Asp Ala Ile Arg Leu Lys Lys Lys
    1610   1615   1620

20

Met Glu Gly Asp Leu Asn Glu Met Glu Ile Gln Leu Asn His Ala
    1625   1630   1635

25

Asn Arg Met Ala Ala Glu Ala Leu Arg Asn Tyr Arg Asn Thr Gln
    1640   1645   1650

30   Gly Ile Leu Lys Asp Thr Gln Ile His Leu Asp Asp Ala Leu Arg
         1655   1660   1665

Ser Gln Glu Asp Leu Lys Glu Gln Leu Ala Met Val Glu Arg Arg
    1670   1675   1680
35

Ala Asn Leu Leu Gln Ala Glu Ile Glu Glu Leu Arg Ala Thr Leu
    1685   1690   1695

40

Glu Gln Thr Glu Arg Ser Arg Lys Ile Ala Glu Gln Glu Leu Leu
    1700   1705   1710

45

Asp Ala Ser Glu Arg Val Gln Leu Leu His Thr Gln Asn Thr Ser
    1715   1720   1725

```
      Leu Ile  Asn Thr Lys Lys Lys  Leu Glu Thr Asp Ile  Ser Gln Met
          1730              1735              1740

  5

      Gln Gly  Glu Met Glu Asp Ile  Leu Gln Glu Ala Arg  Asn Ala Glu
          1745              1750              1755

 10   Glu Lys  Ala Lys Lys Ala Ile  Thr Asp Ala Ala Met  Met Ala Glu
          1760              1765              1770

      Glu Leu  Lys Lys Glu Gln Asp  Thr Ser Ala His Leu  Glu Arg Met
 15       1775              1780              1785

      Lys Lys  Asn Met Glu Gln Thr  Val Lys Asp Leu Gln  Leu Arg Leu
          1790              1795              1800
 20

      Asp Glu  Ala Glu Gln Leu Ala  Leu Lys Gly Gly Lys  Lys Gln Ile
          1805              1810              1815

 25
      Gln Lys  Leu Glu Ala Arg Val  Arg Glu Leu Glu Gly  Glu Val Glu
          1820              1825              1830

 30   Ser Glu  Gln Lys Arg Asn Ala  Glu Ala Val Lys Gly  Leu Arg Lys
          1835              1840              1845

      His Glu  Arg Arg Val Lys Glu  Leu Thr Tyr Gln Thr  Glu Glu Asp
 35       1850              1855              1860

      Arg Lys  Asn Ile Leu Arg Leu  Gln Asp Leu Val Asp  Lys Leu Gln
          1865              1870              1875
 40

      Ala Lys  Val Lys Ser Tyr Lys  Arg Gln Ala Glu Glu  Ala Glu Glu
          1880              1885              1890

 45
      Gln Ser  Asn Thr Asn Leu Ala  Lys Phe Arg Lys Leu  Gln His Glu
          1895              1900              1905
```

Leu Glu Glu Ala Glu Glu Arg Ala Asp Ile Ala Glu Ser Gln Val
     1910   1915   1920

5

Asn Lys Leu Arg Val Lys Ser Arg Glu Val His Thr Lys Val Ile
     1925   1930   1935

10 Ser Glu Glu
        1940

    <210> 3
15 <211> 6016
    <212> DNA
    <213> Homo sapiens

    <400> 3
20 atccttcctc aaaattcttg aagtagttgt ctgctttgag cctgccacct tcttcatctg   60

    ataatacaag aggtatacct agtccagcac tgccatcaat aacctgcagc catgagttct   120

    gactctgaga tggccatttt tggggaggct gctcctttcc tccgaaagtc tgaaaaggag   180
25

    cgaattgaag ctcagaacaa gccttttgat gccaagacat cagtctttgt ggtggaccct   240

    aaggagtcct acgtgaaagc aatagtgcag agcagggaag ggggggaaggt gacagccaag   300

30 accgaagctg gagctactgt aactgtgaaa gaagaccaag tcttctccat gaaccctccc   360

    aaatatgaca agatcgagga catggccatg atgactcacc tgcatgagcc tgctgtgctg   420

    tataacctca aagagcgtta cgcagcctgg atgatctaca cctactcggg cctcttctgt   480
35

    gtcaccgtca accCCtacaa gtggctgccg gtgtacaacc ctgaggtggt gacagcctac   540

    cgaggcaaaa agcgccagga ggccccaccc catatcttct ccatctctga caatgcctat   600

40 cagttcatgc taactgatcg tgaaaaccag tcaatcttga ttactggaga atctggtgca   660

    gggaagactg tgaacacgaa gcgtgtcatc cagtactttg caacaattgc agttactgga   720

    gagaagaaaa aagaggaacc tgcctctggc aaaatgcagg ggaccCttga agatcaaatc   780
45

    atcagtgcta accCCCtact ggaagccttc ggcaatgcca agaccgtgag gaatgacaac   840

    tcctctcgct ttggtaaatt catcaggatc catttTggtg ccacaggcaa actggcttct   900

```
       gcagatattg aaacatatct gctagagaag tcccgagtta cttttcagct aaaggctgaa    960

  5    agaagctacc acatatttta tcaaatcctg tccaataaga aaccagagct cattgaaatg   1020

       cttctgatca ccaccaaccc atatgacttc gcatttgtca gccaagggga aattactgtg   1080

       cccagcattg atgaccagga agagctgatg gccacagata gtgctgtgga catcctgggt   1140

 10    ttcactgctg atgaaaaggt ggccatttac aagctcactg gagccgtgat gcattatggg   1200

       aacatgaaat tcaagcaaaa gcaaagggaa gagcaggcag agccagatgg cacggaagtt   1260

 15    gctgacaaag ctgcttatct gacaagtctg aactctgctg acctgctcaa atctctctgc   1320

       tatcccagag tcaaggtcgg caatgagttc gtaaccaaag gccagactgt gcagcaggtg   1380

       tacaacgcag tgggtgctct ggccaaagcc atctacgaga agatgttcct gtggatggtc   1440

 20    acccgcatca accagcagct ggacaccaag cagcccaggc agtacttcat cggggtcttg   1500

       gacattgctg gctttgagat ctttgatttc aacagcctgg agcagctgtg catcaacttc   1560

 25    accaacgaga aactgcaaca gttttttcaac caccacatgt tcgtgctgga gcaggaagag   1620

       tacaagaagg aaggcatcga gtgggagttc attgacttcg ggatggacct ggctgcctgc   1680

       atcgagctca tcgagaagcc tatgggcatc ttctccatcc tagaagagga gtgcatgttc   1740

 30    cccaaggcaa cagacacctc cttcaagaac aagctgtatg aacaacatct tggaaaatcc   1800

       aacaacttcc agaagcccaa gcctgccaaa ggcaagcctg aggctcactt ctcactggtg   1860

 35    cactatgccg gcaccgtgga ctacaacatc gccggctggc tggacaaaaa caaggacccc   1920

       ctgaatgaga ctgtggtggg gctgtaccag aagtctgcaa tgaagactct ggctttcctc   1980

       ttctctgggg cacaaactgc tgaagcagag ggtggtggtg gaaagaaagg tggcaaaaag   2040

 40    aagggttctt ctttccagac agtgtcagct cttttcaggg agaatttgaa taagctgatg   2100

       accaacttga ggagcactca cccccacttt gtgcggtgca tcatccccaa tgaaactaaa   2160

       actcctggtg ccatggagca tgagcttgtc ctgcatcagc tgaggtgtaa cggtgtgctg   2220

 45    gaaggcatcc gcatctgcag gaaaggcttc ccaagcagaa tcctttatgc agacttcaaa   2280

       cagagataca aggttctaaa tgcgagtgct atcccagagg gtcagttcat tgacagcaag   2340
```

```
     aaggcttctg agaaacttct agggtctatt gaaattgacc acacccagta caaattcggt   2400

     cataccaagg ttttcttcaa agctggcctg ctgggaactc tagaagaaat gcgagatgaa   2460
5
     aagctagctc aactcatcac gcgcactcaa gccatatgca gggggttcct gatgagagtg   2520

     gagttcagaa agatgatgga gaggagagag tccatcttct gcattcagta caacatccgt   2580

10   gctttcatga atgtgaagca ctggccctgg atgaagctgt atttcaagat caagcccctc   2640

     ctcaagagtg cagagacaga gaaggagatg gccaacatga aggaagaatt tgagaaaacc   2700

     aaagaagagc tggctaagac agaggcaaaa aggaaagaac tagaagaaaa gatggtgacg   2760
15
     ctaatgcaag agaaaaatga cttacaactc caagttcaag ctgaagcaga tgccttggct   2820

     gatgcagagg aaagatgtga tcagttgatt aaaaccaaaa tccaacttga ggccaaaatc   2880

20   aaagaggtaa ctgaaagagc tgaggatgag gaagagatca atgctgagct gacagccaag   2940

     aagaggaaac tggaggatga atgttcagag ctcaagaaag acattgatga ccttgagctg   3000

     acactggcca aggttgagaa ggagaaacat gccacagaga acaaggtgaa aaacctcaca   3060
25
     gaagagatgg caggtctgga tgaaaccatt gctaagctga ccaaggagaa gaaggctctc   3120

     caggaggccc accagcagac cctggatgac ctgcagatgg aggaggacaa agtcaacacc   3180

30   ctgaccaaag ctaaaaccaa gctagaacag caagtggacg atcttgaagg atctctggaa   3240

     caagaaaaga aactttgcat ggacttagaa agagccaaga gaaaactgga gggtgaccta   3300

     aaattggccc aagaatccac aatggataca gaaaatgaca aacagcaact taatgagaaa   3360
35
     ctcaaaaaga aagagtttga aatgagcaat ctgcaaggca agattgaaga tgaacaagcc   3420

     cttgcaatgc agctacaaaa gaagatcaaa gaattacagg cccgcattga ggagctggag   3480

40   gaggaaatcg aggcagagcg ggcctcccgg gccaaagcag aaaagcagcg ctctgacctc   3540

     tcccgggagc tggaggagat cagtgagagg ctggaagaag ccggtggggc cacttcagcc   3600

     cagattgagt tgaacaagaa gcgggaggct gagttccaga aaatgcgcag ggacctggaa   3660
45
     gagtccaccc tgcagcacga agccacggca gctgctcttc ggaagaagca cgcagatagt   3720

     gtggctgagc ttgggaagca gatcgacagc cttcagcggg tcaagcagaa gctggagaag   3780
```

```
     gaaaagagtg agctgaagat ggagatcaat gaccttgcta gtaacatgga gactgtctcc   3840

     aaagccaagg caaactttga gaaaatgtgc cgcaccctag aggaccagct tagtgaaata   3900
 5
     aaaacaaagg aagaagagca gcaacgctta ataaatgagt tgtcagccca gaaggcacgt   3960

     ttacacacag aatcaggtga gttttcacga cagctagatg aaaaagatgc tatggtttct   4020

10   cagctatccc gaggcaaaca agcatttaca caacagattg aagaattaaa gaggcagcta   4080

     gaagaggaga ctaaggccaa gagcactctg gcccatgccc tgcagtcagc ccgccatgac   4140

     tgtgacctgc tgcgggaaca gtatgaggag gagcaggaag ccaaggctga gctgcagagg   4200
15
     ggaatgtcca aggccaacag tgaggttgcc cagtggagga ccaagtacga gacggacgcc   4260

     atccagcgca cagaggagct ggaggaggcc aagaagaagc tagcccagcg tctgcaggat   4320

20   gcagaagaac atgtagaagc tgtgaattcc aaatgtgctt ctcttgaaaa gacaaagcag   4380

     aggctacaga atgaagtaga ggacctcatg attgatgtgg aacgatctaa tgctgcctgc   4440

     atagctctcg ataagaagca aagaaacttt gacaaggttc tggcagaatg gaaacagaag   4500
25
     tatgaggaaa ctcaggctga acttgaggcc tcccagaagg agtcgcgttc tctcagcact   4560

     gagctgttca aggtgaagaa tgcctacgag gaatccctgg atcatcttga aactctaaag   4620

30   cgagagaata agaacttaca acaggagatt tctgacctga cagagcaaat tgcagagggt   4680

     ggaaagcata tccatgaact ggagaaagta aagaaacaac ttgatcatga gaagagtgaa   4740

     ctacagactt ccctagagga agcagaggca tctcttgagc atgaagaagg caaaattctt   4800
 35
     cgcattcaac ttgagctaaa tcaggtgaaa tctgagattg accgaaaaat tgctgaaaaa   4860

     gatgaagaac tcgatcagct aaagaggaac catctcagag ttgtggagtc aatgcagagt   4920

40   acactggatg ctgagatcag gagcagaaat gatgctctga ggatcaagaa gaagatggag   4980

     ggagatctta atgaaatgga aatccagctg aaccatgcca accgccaggc tgctgaggca   5040

     ctaaggaatc ttagaaacac acaaggaata ctgaaggaca ctcagctaca tttggatgat   5100
45
     gccatcagag gccaagatga ccttaaggaa caattggcaa tggttgagcg cagagctaac   5160

     ctgatgcagg ctgaagttga agagctcagg gcatccctgg aacggactga gagaggcagg   5220
```

```
        aaaatggcag agcaagagct tctggatgcc agtgaacgtg tgcaacttct gcacactcag    5280

        aacaccagcc tgatcaacac caagaagaag ctggaaacag acatttccca aatccaggga    5340

        gagatggagg acatcgtcca ggaagcccgc aatgcagagg agaaggccaa gaaggccatc    5400

        actgatgctg ccatgatggc tgaggagctg aagaaggaac aggacaccag cgcccacctg    5460

        gagcggatga agaagaacat ggagcagacc gtgaaggatc tgcagctccg tctgggtgag    5520

        gctgagcagc tggcgctgaa gggtgggaag aagcagatcc agaaactgga ggccagggtg    5580

        agagagcttg aaagtgaggt ggaaagtgaa cagaagcaca atgttgaggc tgtcaagggt    5640

        cttcgcaaac atgagagaag agtgaaggaa ctcacttacc agactgagga ggaccgcaag    5700

        aatattctca ggctgcagga cttggtggac aaattgcaaa ccaaagtcaa agcttacaag    5760

        agacaagctg aagaggctga ggaacaatcc aatgtcaacc ttgccaagtt ccgcaagctc    5820

        cagcacgagc tggaggaggc cgaggaacgg gctgacattg ctgagtccca agtcaacaag    5880

        ctgagagtga agagtcggga ggttcacaca aaagtcataa gtgaagagta attcattcta    5940

        atgaaagaaa atgtgaccaa agaaatgcac gaaatgtgaa gttctttgtc actgtcctgt    6000

        atatcaagga aataaa                                                    6016
```

<210> 4
<211> 1939
<212> PRT
<213> Homo sapiens

<400> 4

Met Ser Ser Asp Ser Glu Met Ala Ile Phe Gly Glu Ala Ala Pro Phe
1   5   10   15

Leu Arg Lys Ser Glu Lys Glu Arg Ile Glu Ala Gln Asn Lys Pro Phe
                20   25   30

Asp Ala Lys Thr Ser Val Phe Val Val Asp Pro Lys Glu Ser Tyr Val
                35   40   45

Lys Ala Ile Val Gln Ser Arg Glu Gly Gly Lys Val Thr Ala Lys Thr
    50   55   60

5

Glu Ala Gly Ala Thr Val Thr Val Lys Glu Asp Gln Val Phe Ser Met
65   70   75   80

10 Asn Pro Pro Lys Tyr Asp Lys Ile Glu Asp Met Ala Met Met Thr His
                    85   90   95

Leu His Glu Pro Ala Val Leu Tyr Asn Leu Lys Glu Arg Tyr Ala Ala
15   100   105   110

Trp Met Ile Tyr Thr Tyr Ser Gly Leu Phe Cys Val Thr Val Asn Pro
            115   120   125
20

Tyr Lys Trp Leu Pro Val Tyr Asn Pro Glu Val Val Thr Ala Tyr Arg
    130   135   140

25

Gly Lys Lys Arg Gln Glu Ala Pro Pro His Ile Phe Ser Ile Ser Asp
145   150   155   160

30 Asn Ala Tyr Gln Phe Met Leu Thr Asp Arg Glu Asn Gln Ser Ile Leu
                165   170   175

Ile Thr Gly Glu Ser Gly Ala Gly Lys Thr Val Asn Thr Lys Arg Val
35   180   185   190

Ile Gln Tyr Phe Ala Thr Ile Ala Val Thr Gly Glu Lys Lys Lys Glu
        195   200   205
40

Glu Pro Ala Ser Gly Lys Met Gln Gly Thr Leu Glu Asp Gln Ile Ile
    210   215   220

45

Ser Ala Asn Pro Leu Leu Glu Ala Phe Gly Asn Ala Lys Thr Val Arg
225   230   235   240

Asn Asp Asn Ser Ser Arg Phe Gly Lys Phe Ile Arg Ile His Phe Gly
             245   250   255

5

Ala Thr Gly Lys Leu Ala Ser Ala Asp Ile Glu Thr Tyr Leu Leu Glu
          260   265   270

10 Lys Ser Arg Val Thr Phe Gln Leu Lys Ala Glu Arg Ser Tyr His Ile
        275   280   285

Phe Tyr Gln Ile Leu Ser Asn Lys Lys Pro Glu Leu Ile Glu Met Leu
15   290   295   300

Leu Ile Thr Thr Asn Pro Tyr Asp Phe Ala Phe Val Ser Gln Gly Glu
305   310   315   320
20

Ile Thr Val Pro Ser Ile Asp Asp Gln Glu Glu Leu Met Ala Thr Asp
         325   330   335

25

Ser Ala Val Asp Ile Leu Gly Phe Thr Ala Asp Glu Lys Val Ala Ile
        340   345   350

30 Tyr Lys Leu Thr Gly Ala Val Met His Tyr Gly Asn Met Lys Phe Lys
        355   360   365

Gln Lys Gln Arg Glu Glu Gln Ala Glu Pro Asp Gly Thr Glu Val Ala
35   370   375   380

Asp Lys Ala Ala Tyr Leu Thr Ser Leu Asn Ser Ala Asp Leu Leu Lys
385   390   395   400
40

Ser Leu Cys Tyr Pro Arg Val Lys Val Gly Asn Glu Phe Val Thr Lys
        405   410   415

45

Gly Gln Thr Val Gln Gln Val Tyr Asn Ala Val Gly Ala Leu Ala Lys
        420   425   430

Ala Ile Tyr Glu Lys Met Phe Leu Trp Met Val Thr Arg Ile Asn Gln
    435   440   445

5

Gln Leu Asp Thr Lys Gln Pro Arg Gln Tyr Phe Ile Gly Val Leu Asp
    450   455   460

10 Ile Ala Gly Phe Glu Ile Phe Asp Phe Asn Ser Leu Glu Gln Leu Cys
    465   470   475   480

Ile Asn Phe Thr Asn Glu Lys Leu Gln Gln Phe Phe Asn His His Met
15   485   490   495

Phe Val Leu Glu Gln Glu Glu Tyr Lys Lys Glu Gly Ile Glu Trp Glu
        500   505   510
20

Phe Ile Asp Phe Gly Met Asp Leu Ala Ala Cys Ile Glu Leu Ile Glu
        515   520   525

25

Lys Pro Met Gly Ile Phe Ser Ile Leu Glu Glu Glu Cys Met Phe Pro
    530   535   540

30 Lys Ala Thr Asp Thr Ser Phe Lys Asn Lys Leu Tyr Glu Gln His Leu
    545   550   555   560

Gly Lys Ser Asn Asn Phe Gln Lys Pro Lys Pro Ala Lys Gly Lys Pro
            565   570   575
35

Glu Ala His Phe Ser Leu Val His Tyr Ala Gly Thr Val Asp Tyr Asn
            580   585   590
40

Ile Ala Gly Trp Leu Asp Lys Asn Lys Asp Pro Leu Asn Glu Thr Val
        595   600   605

45

Val Gly Leu Tyr Gln Lys Ser Ala Met Lys Thr Leu Ala Phe Leu Phe
        610   615   620

Ser Gly Ala Gln Thr Ala Glu Ala Glu Gly Gly Gly Gly Lys Lys Gly
625   630   635   640

5

Gly Lys Lys Lys Gly Ser Ser Phe Gln Thr Val Ser Ala Leu Phe Arg
                645   650   655

10 Glu Asn Leu Asn Lys Leu Met Thr Asn Leu Arg Ser Thr His Pro His
                    660   665   670

Phe Val Arg Cys Ile Ile Pro Asn Glu Thr Lys Thr Pro Gly Ala Met
15   675   680   685

Glu His Glu Leu Val Leu His Gln Leu Arg Cys Asn Gly Val Leu Glu
        690   695   700
20

Gly Ile Arg Ile Cys Arg Lys Gly Phe Pro Ser Arg Ile Leu Tyr Ala
705   710   715   720

25

Asp Phe Lys Gln Arg Tyr Lys Val Leu Asn Ala Ser Ala Ile Pro Glu
                725   730   735

30 Gly Gln Phe Ile Asp Ser Lys Lys Ala Ser Glu Lys Leu Leu Gly Ser
                740   745   750

Ile Glu Ile Asp His Thr Gln Tyr Lys Phe Gly His Thr Lys Val Phe
35   755   760   765

Phe Lys Ala Gly Leu Leu Gly Thr Leu Glu Glu Met Arg Asp Glu Lys
        770   775   780
40

Leu Ala Gln Leu Ile Thr Arg Thr Gln Ala Ile Cys Arg Gly Phe Leu
785   790   795   800

45

Met Arg Val Glu Phe Arg Lys Met Met Glu Arg Arg Glu Ser Ile Phe
                805   810   815

Cys Ile Gln Tyr Asn Ile Arg Ala Phe Met Asn Val Lys His Trp Pro
820   825   830

5

Trp Met Lys Leu Tyr Phe Lys Ile Lys Pro Leu Leu Lys Ser Ala Glu
835   840   845

10   Thr Glu Lys Glu Met Ala Asn Met Lys Glu Glu Phe Glu Lys Thr Lys
850   855   860

Glu Glu Leu Ala Lys Thr Glu Ala Lys Arg Lys Glu Leu Glu Glu Lys
15   865   870   875   880

Met Val Thr Leu Met Gln Glu Lys Asn Asp Leu Gln Leu Gln Val Gln
885   890   895
20

Ala Glu Ala Asp Ala Leu Ala Asp Ala Glu Glu Arg Cys Asp Gln Leu
900   905   910

25

Ile Lys Thr Lys Ile Gln Leu Glu Ala Lys Ile Lys Glu Val Thr Glu
915   920   925

30   Arg Ala Glu Asp Glu Glu Glu Ile Asn Ala Glu Leu Thr Ala Lys Lys
930   935   940

Arg Lys Leu Glu Asp Glu Cys Ser Glu Leu Lys Lys Asp Ile Asp Asp
35   945   950   955   960

Leu Glu Leu Thr Leu Ala Lys Val Glu Lys Glu Lys His Ala Thr Glu
965   970   975
40

Asn Lys Val Lys Asn Leu Thr Glu Glu Met Ala Gly Leu Asp Glu Thr
980   985   990

45

Ile Ala Lys Leu Thr Lys Glu Lys Lys Ala Leu Gln Glu Ala His Gln
995   1000   1005

Gln Thr Leu Asp Asp Leu Gln Met Glu Glu Asp Lys Val Asn Thr
    1010   1015   1020

5

Leu Thr Lys Ala Lys Thr Lys Leu Glu Gln Gln Val Asp Asp Leu
    1025   1030   1035

10   Glu Gly Ser Leu Glu Gln Glu Lys Lys Leu Cys Met Asp Leu Glu
        1040   1045   1050

Arg Ala Lys Arg Lys Leu Glu Gly Asp Leu Lys Leu Ala Gln Glu
15   1055   1060   1065

Ser Thr Met Asp Thr Glu Asn Asp Lys Gln Gln Leu Asn Glu Lys
        1070   1075   1080
20

Leu Lys Lys Lys Glu Phe Glu Met Ser Asn Leu Gln Gly Lys Ile
        1085   1090   1095

25

Glu Asp Glu Gln Ala Leu Ala Met Gln Leu Gln Lys Lys Ile Lys
        1100   1105   1110

30   Glu Leu Gln Ala Arg Ile Glu Glu Leu Glu Glu Glu Ile Glu Ala
        1115   1120   1125

Glu Arg Ala Ser Arg Ala Lys Ala Glu Lys Gln Arg Ser Asp Leu
35   1130   1135   1140

Ser Arg Glu Leu Glu Glu Ile Ser Glu Arg Leu Glu Glu Ala Gly
        1145   1150   1155
40

Gly Ala Thr Ser Ala Gln Ile Glu Leu Asn Lys Lys Arg Glu Ala
        1160   1165   1170

45

Glu Phe Gln Lys Met Arg Arg Asp Leu Glu Glu Ser Thr Leu Gln
        1175   1180   1185

His Glu Ala Thr Ala Ala Ala Leu Arg Lys Lys His Ala Asp Ser
    1190   1195   1200

5

Val Ala Glu Leu Gly Lys Gln Ile Asp Ser Leu Gln Arg Val Lys
    1205   1210   1215

10 Gln Lys Leu Glu Lys Glu Lys Ser Glu Leu Lys Met Glu Ile Asn
      1220   1225   1230

Asp Leu Ala Ser Asn Met Glu Thr Val Ser Lys Ala Lys Ala Asn
15   1235   1240   1245

Phe Glu Lys Met Cys Arg Thr Leu Glu Asp Gln Leu Ser Glu Ile
    1250   1255   1260
20

Lys Thr Lys Glu Glu Glu Gln Gln Arg Leu Ile Asn Glu Leu Ser
    1265   1270   1275

25

Ala Gln Lys Ala Arg Leu His Thr Glu Ser Gly Glu Phe Ser Arg
    1280   1285   1290

30 Gln Leu Asp Glu Lys Asp Ala Met Val Ser Gln Leu Ser Arg Gly
      1295   1300   1305

Lys Gln Ala Phe Thr Gln Gln Ile Glu Glu Leu Lys Arg Gln Leu
35   1310   1315   1320

Glu Glu Glu Thr Lys Ala Lys Ser Thr Leu Ala His Ala Leu Gln
    1325   1330   1335
40

Ser Ala Arg His Asp Cys Asp Leu Leu Arg Glu Gln Tyr Glu Glu
    1340   1345   1350

45

Glu Gln Glu Ala Lys Ala Glu Leu Gln Arg Gly Met Ser Lys Ala
    1355   1360   1365

Asn Ser Glu Val Ala Gln Trp Arg Thr Lys Tyr Glu Thr Asp Ala
    1370   1375   1380

5

Ile Gln Arg Thr Glu Glu Leu Glu Glu Ala Lys Lys Lys Leu Ala
    1385   1390   1395

10 Gln Arg Leu Gln Asp Ala Glu Glu His Val Glu Ala Val Asn Ser
        1400   1405   1410

Lys Cys Ala Ser Leu Glu Lys Thr Lys Gln Arg Leu Gln Asn Glu
15   1415   1420   1425

Val Glu Asp Leu Met Ile Asp Val Glu Arg Ser Asn Ala Ala Cys
    1430   1435   1440
20

Ile Ala Leu Asp Lys Lys Gln Arg Asn Phe Asp Lys Val Leu Ala
    1445   1450   1455

25
Glu Trp Lys Gln Lys Tyr Glu Glu Thr Gln Ala Glu Leu Glu Ala
    1460   1465   1470

30 Ser Gln Lys Glu Ser Arg Ser Leu Ser Thr Glu Leu Phe Lys Val
        1475   1480   1485

Lys Asn Ala Tyr Glu Glu Ser Leu Asp His Leu Glu Thr Leu Lys
35   1490   1495   1500

Arg Glu Asn Lys Asn Leu Gln Gln Glu Ile Ser Asp Leu Thr Glu
    1505   1510   1515
40

Gln Ile Ala Glu Gly Gly Lys His Ile His Glu Leu Glu Lys Val
    1520   1525   1530

45
Lys Lys Gln Leu Asp His Glu Lys Ser Glu Leu Gln Thr Ser Leu
    1535   1540   1545

Glu Glu Ala Glu Ala Ser Leu Glu His Glu Glu Gly Lys Ile Leu
    1550   1555   1560

5

Arg Ile Gln Leu Glu Leu Asn Gln Val Lys Ser Glu Ile Asp Arg
    1565   1570   1575

10 Lys Ile Ala Glu Lys Asp Glu Glu Leu Asp Gln Leu Lys Arg Asn
        1580   1585   1590

His Leu Arg Val Val Glu Ser Met Gln Ser Thr Leu Asp Ala Glu
15   1595   1600   1605

Ile Arg Ser Arg Asn Asp Ala Leu Arg Ile Lys Lys Lys Met Glu
    1610   1615   1620

20

Gly Asp Leu Asn Glu Met Glu Ile Gln Leu Asn His Ala Asn Arg
    1625   1630   1635

25

Gln Ala Ala Glu Ala Leu Arg Asn Leu Arg Asn Thr Gln Gly Ile
    1640   1645   1650

30 Leu Lys Asp Thr Gln Leu His Leu Asp Asp Ala Ile Arg Gly Gln
        1655   1660   1665

Asp Asp Leu Lys Glu Gln Leu Ala Met Val Glu Arg Arg Ala Asn
35   1670   1675   1680

Leu Met Gln Ala Glu Val Glu Glu Leu Arg Ala Ser Leu Glu Arg
    1685   1690   1695

40

Thr Glu Arg Gly Arg Lys Met Ala Glu Gln Glu Leu Leu Asp Ala
    1700   1705   1710

45

Ser Glu Arg Val Gln Leu Leu His Thr Gln Asn Thr Ser Leu Ile
    1715   1720   1725

Asn Thr Lys Lys Lys Leu Glu Thr Asp Ile Ser Gln Ile Gln Gly
     1730   1735   1740

5

Glu Met Glu Asp Ile Val Gln Glu Ala Arg Asn Ala Glu Glu Lys
     1745   1750   1755

10   Ala Lys Lys Ala Ile Thr Asp Ala Ala Met Met Ala Glu Glu Leu
          1760   1765   1770

Lys Lys Glu Gln Asp Thr Ser Ala His Leu Glu Arg Met Lys Lys
15   1775   1780   1785

Asn Met Glu Gln Thr Val Lys Asp Leu Gln Leu Arg Leu Gly Glu
     1790   1795   1800
20

Ala Glu Gln Leu Ala Leu Lys Gly Gly Lys Lys Gln Ile Gln Lys
     1805   1810   1815

25

Leu Glu Ala Arg Val Arg Glu Leu Glu Ser Glu Val Glu Ser Glu
     1820   1825   1830

30   Gln Lys His Asn Val Glu Ala Val Lys Gly Leu Arg Lys His Glu
          1835   1840   1845

Arg Arg Val Lys Glu Leu Thr Tyr Gln Thr Glu Glu Asp Arg Lys
35   1850   1855   1860

Asn Ile Leu Arg Leu Gln Asp Leu Val Asp Lys Leu Gln Thr Lys
     1865   1870   1875
40

Val Lys Ala Tyr Lys Arg Gln Ala Glu Glu Ala Glu Glu Gln Ser
     1880   1885   1890

45

Asn Val Asn Leu Ala Lys Phe Arg Lys Leu Gln His Glu Leu Glu
     1895   1900   1905

Glu Ala Glu Glu Arg Ala Asp Ile Ala Glu Ser Gln Val Asn Lys
    1910   1915   1920

5

Leu Arg Val Lys Ser Arg Glu Val His Thr Lys Val Ile Ser Glu
    1925   1930   1935

10 Glu

<210> 5
15 <211> 5925
<212> DNA
<213> Homo sapiens

<400> 5
20 atgagttctg actctgagat ggccattttt ggggaggctg ctcctttcct ccgaaagtct   60

    gaaagggagc gaattgaagc ccagaacaag ccttttgatg ccaagacatc agtctttgtg   120

    gtggacccta aggagtcctt tgtgaaagca acagtgcaga gcagggaagg ggggaaggtg   180
25

    acagctaaga ccgaagctgg agctactgta acagtgaaag atgaccaagt cttccccatg   240

    aaccctccca aatatgacaa gatcgaggac atggccatga tgactcatct acacgagcct   300

30 gctgtgctgt acaacctcaa agagcgctac gcagcctgga tgatctacac ctactcaggc   360

    ttgttctgtg tcactgtcaa cccctacaag tggttgccag tgtataatgc agaagtggtg   420

    acagcctacc gaggcaaaaa gcgccaggaa gccccacccc acatcttctc catctctgac   480
35

    aatgcctatc agttcatgct gactgatcgg gagaatcagt ctatcttgat caccggagaa   540

    tctggcgcag ggaagactgt gaacaccaag cgtgtcatcc agtactttgc aacaattgca   600

40 gttactgggg agaagaagaa ggaagaagtt acttctggca aaatgcaggg gactctggaa   660

    gatcaaatca tcagtgccaa ccccctactg gaggcctttg gcaacgccaa gaccgtgagg   720

    aatgacaact cctctcgctt tggtaaattc atcaggatcc acttcggtac cacagggaaa   780
45

    ctggcttctg ctgatattga aacatatctt ctggagaagt ctagagttac tttccagcta   840

    aaggctgaaa gaagctatca tattttttat cagatcatgt ctaacaagaa gccagatcta   900

attgaaatgc tcctgatcac caccaaccca tacgattatg ccttcgtcag tcaaggggag   960

atcacagtgc ccagcattga tgaccaagaa gagttgatgg ctacagatag tgccattgaa   1020

attctgggct ttacttcaga tgaaagagtg tccatctata agctcacagg ggctgtgatg   1080

cattatggga acatgaaatt caagcaaaag cagcgtgagg agcaagctga gccagatggc   1140

actgaagttg ctgacaaggc agcctatctc caaaatctga actctgcaga tctgctcaaa   1200

gccctctgct accctagggt caaggtcggc aatgagtatg tcaccaaagg tcaaactgtg   1260

cagcaggtgt acaatgcagt gggtgctctg gccaaagctg tctacgataa gatgttcttg   1320

tggatggtca cccgcatcaa ccagcagctg gacaccaagc agcccaggca gtacttcatt   1380

ggggtcttgg acattgctgg ctttgagatc tttgatttca acagcctgga gcagctgtgc   1440

atcaacttca ccaatgagaa actgcaacag ttttttcaacc accacatgtt cgtgctggag   1500

caggaggagt acaagaagga aggcattgag tggacgttca ttgactttgg gatggacctg   1560

gctgcctgca tcgagctcat cgagaagcct atgggcatct tctccatcct ggaagaggag   1620

tgcatgttcc ccaaggcgac agacacctcc ttcaagaaca agctgtatga acaacatctt   1680

ggaaaatcca ataacttcca gaagcccaag cctgccaaag gcaagcctga ggcccacttc   1740

tctttgattc actatgctgg caccgtggac tacaacattg ccggctggct tgacaagaac   1800

aaggaccccc tgaatgagac tgtggtgggg ctgtaccaga agtctgcaat gaagactctg   1860

gctctcctct ttgttggggc aacgggagcg gaagcagagg ctggcggtgg aaagaaaggt   1920

ggtaagaaga agggttcttc tttccagact gtgtcggctc tcttcaggga gaatttgaat   1980

aagctgatga ccaacttgag gagcactcac ccccactttg tgcggtgcat catccccaat   2040

gaaactaaaa ctcctggtgc catggagcat gagcttgtcc tgcatcagct gaggtgtaac   2100

ggtgtgctgg aaggcatccg catctgcagg aaaggcttcc caagcagaat cctttatgca   2160

gacttcaaac agagatacaa ggtgttaaat gcaagtgcta tccctgaagg acaattcatc   2220

gatagcaaga aggcttcaga gaagctcctg gggtccattg acattgacca cacccagtat   2280

aaatttggtc acaccaaggt cttttttcaaa gctggtcttc tggggctcct agaggagatg   2340

```
      cgagatgaga agctggccca gctgattacc cgaacccagg ccatgtgcag agggttcttg   2400

      gcaagagtgg agtaccagaa aatggtggaa agaagagagt ccatcttctg catccagtac   2460
 5
      aatgtccgtg ccttcatgaa tgtcaagcac tggccctgga tgaagctgta tttcaagatc   2520

      aaacccctcc tcaaaagtgc agagacagag aaggagatgg ccaacatgaa ggaagaattt   2580

10    gagaaaacca aagaagagct ggctaagacc gaggcaaaaa ggaaagagct ggaagaaaaa   2640

      atggtgactc tgatgcaaga aaaaaatgac ttgcaactcc aggttcaagc tgaagctgac   2700

      agcttggctg atgcagagga aaggtgtgac cagctaatca aaaccaaaat ccagctagaa   2760
15
      gccaaaatca aagaggtgac tgagagagct gaggatgagg aagagatcaa tgctgagctg   2820

      acagccaaga agaggaaact ggaggatgaa tgttcagaac tcaagaaaga cattgatgac   2880

20    cttgagctga cactggccaa ggttgagaag gagaaacatg ccacagaaaa caaggtgaaa   2940

      aacctcacag aagagatggc gggtctggat gaaaccattg ctaagctgac caaggagaag   3000

      aaggctctcc aggaggccca ccagcagacc ctggatgacc tgcaggcaga ggaggacaaa   3060
25
      gtcaacaccc tgaccaaagc taaaatcaaa cttgaacaac aagtggatga tcttgaagga   3120

      tctttggaac aagaaaagaa aatccggatg gatctagaaa gagcaaagag aaaactagag   3180

30    ggagacctaa aattggctca agaatccgca atggatatag aaaatgacaa acaacaactt   3240

      gatgaaaagc ttaaaaagaa agagtttgaa atgagcggtc tgcaaagcaa gattgaagat   3300

      gaacaagccc ttggtatgca gctgcagaag aaaatcaagg agttacaagc ccgcattgag   3360
35
      gagctggagg aggaaatcga ggcagagcgg gcctcccggg ccaaagcaga gaagcagcgc   3420

      tctgatctct cccgggagct ggaggagatc agtgagaggc tggaagaagc cggtggggcc   3480

40    acctcggccc agattgagat gaacaagaag cgggaagctg agttccagaa aatgcgcagg   3540

      gacctggagg aggccaccct acagcatgag gccacggcgg ccaccctgag gaagaagcat   3600

      gcagatagtg tggccgagct tggggagcag attgacaacc tgcagcgagt gaagcagaag   3660
45
      ctggagaagg agaagagtga gatgaagatg gagatcgatg accttgctag taacatggag   3720

      actgtctcca aagccaaggg aaaccttgaa aagatgtgcc gcgctctaga agatcaactg   3780
```

```
agtgaaatta agaccaagga agaggagcag cagcggctga tcaatgacct cacagcacag   3840

agagcgcgcc tgcaaacaga atcaggtgaa tattcacgcc agctagatga aaaggacaca   3900

ctagtttcac agctctcgag gggcaaacaa gcctttactc aacagattga ggaactgaaa   3960

aggcaacttg aagaggagat aaaggccaag agtgccctgg cacatgccct gcagtcctcc   4020

cgccatgact gtgacctgct gcgggaacag tatgaggagg agcaggaagc caaggccgag   4080

ctacagagag caatgtccaa ggccaacagt gaggttgccc agtggaggac caaatatgag   4140

acagatgcca tccagcgcac agaggagctg gaggaggcca agaagaagct ggctcagcgt   4200

ctgcaggatg ctgaggaaca tgtagaagct gtgaatgcca aatgtgcttc ccttgagaag   4260

acgaagcaga ggctccagaa tgaagttgag gacctcatga ttgatgttga gaggacaaat   4320

gctgcctgtg ccgccctgga caaaaagcaa aggaactttg ataagatcct ggcagaatgg   4380

aaacagaagt gtgaagaaac tcatgctgaa cttgaagctt ctcaaaagga atcccgctca   4440

ctcagcacag aactatttaa gattaagaat gcttatgagg aatctttaga ccaacttgaa   4500

accttgaaac gggaaaataa gaatctgcag caggagattt ctgatctcac tgaacagatt   4560

gcagaaggag gaaagcgcat ccatgaactg gaaaaaataa agaagcaagt tgagcaagaa   4620

aagtctgaac ttcaggctgc cttagaggag gcagaggcat ctcttgaaca tgaagaggga   4680

aagatcctgc gcatccagct tgagttgaac caagtcaagt ctgaggttga taggaaaatt   4740

gctgaaaaag atgaggaaat tgaccagatg aagagaaacc acattagaat cgtggagtcc   4800

atgcagagca cactggatgc tgagatcagg agcaggaatg atgccattag gctcaagaag   4860

aagatggagg gagacctcaa tgaaatggaa atccagctga accatgccaa ccgcatggct   4920

gctgaggccc tgaggaacta taggaacacc caagccatcc tcaaggatac ccagctccac   4980

ctagatgatg ctctccggag ccaagaggac ctgaaggaac agctggctat ggtggagcgc   5040

agagccaacc tgctgcaggc tgagatcgag gaactacgag ccactctgga acagacggag   5100

aggagcagga aaatcgcaga acaggagctc ctggatgcca gtgaacgtgt tcagctcctg   5160

cacacccaga acaccagcct gatcaacacc aagaagaagc tggagacaga catttcccaa   5220
```

```
atccagggag agatggaaga catcatccag gaagcccgca atgcagaaga gaaggccaag   5280

aaggccatca ctgatgctgc catgatggct gaggagctga agaaggaaca ggacaccagc   5340

gcccatctgg agcggatgaa gaagaacttg gaacagacgg tgaaggacct gcagcatcgt   5400

ctggatgagg ctgagcagct ggccctgaag ggtgggaaga agcagatcca gaaactggag   5460

gccagggttc gtgaacttga aggtgaagtt gaaagtgaac agaagcgcaa tgttgaagct   5520

gtcaagggtc tacgcaaaca tgagagaaaa gtgaaggaac tcacttacca aactgaggaa   5580

gaccgcaaga atattctcag gctgcaggac ctggtggaca agctgcaagc aaaggtgaaa   5640

tcctacaaga gacaagctga agaagcggag gaacaatcca acgtcaacct ctccaaattc   5700

cggaggatcc agcacgagct ggaggaggcc gaggaaaggg ctgacattgc tgagtcccag   5760

gtcaacaagc tgagggtgaa gagcagggag gttcacacaa aaatcataag tgaagagtaa   5820

tttatctaac tgctgaaagg tgaccaaaga aatgcacaaa atgtgaaaat ctttgtcact   5880

ccattttgta cttatgactt ttggagataa aaaatttatc tgcca                  5925
```

<210> 6
<211> 1939
<212> PRT
<213> Homo sapiens

<400> 6

```
Met Ser Ser Asp Ser Glu Met Ala Ile Phe Gly Glu Ala Ala Pro Phe
1               5                   10                  15

Leu Arg Lys Ser Glu Arg Glu Arg Ile Glu Ala Gln Asn Lys Pro Phe
                20                  25                  30

Asp Ala Lys Thr Ser Val Phe Val Val Asp Pro Lys Glu Ser Phe Val
            35                  40                  45

Lys Ala Thr Val Gln Ser Arg Glu Gly Gly Lys Val Thr Ala Lys Thr
        50                  55                  60
```

Glu Ala Gly Ala Thr Val Thr Val Lys Asp Asp Gln Val Phe Pro Met
65   70   75   80

5

Asn Pro Pro Lys Tyr Asp Lys Ile Glu Asp Met Ala Met Met Thr His
         85   90   95

10   Leu His Glu Pro Ala Val Leu Tyr Asn Leu Lys Glu Arg Tyr Ala Ala
                  100   105   110

Trp Met Ile Tyr Thr Tyr Ser Gly Leu Phe Cys Val Thr Val Asn Pro
15   115   120   125

Tyr Lys Trp Leu Pro Val Tyr Asn Ala Glu Val Val Thr Ala Tyr Arg
     130   135   140
20

Gly Lys Lys Arg Gln Glu Ala Pro Pro His Ile Phe Ser Ile Ser Asp
145   150   155   .160

25

Asn Ala Tyr Gln Phe Met Leu Thr Asp Arg Glu Asn Gln Ser Ile Leu
         165   170   175

30   Ile Thr Gly Glu Ser Gly Ala Gly Lys Thr Val Asn Thr Lys Arg Val
               180   185   190

Ile Gln Tyr Phe Ala Thr Ile Ala Val Thr Gly Glu Lys Lys Lys Glu
35   195   200   205

Glu Val Thr Ser Gly Lys Met Gln Gly Thr Leu Glu Asp Gln Ile Ile
     210   215   220
40

Ser Ala Asn Pro Leu Leu Glu Ala Phe Gly Asn Ala Lys Thr Val Arg
225   .230   235   240

45

Asn Asp Asn Ser Ser Arg Phe Gly Lys Phe Ile Arg Ile His Phe Gly
         245   250   255

Thr Thr Gly Lys Leu Ala Ser Ala Asp Ile Glu Thr Tyr Leu Leu Glu
        260   265   270

5

Lys Ser Arg Val Thr Phe Gln Leu Lys Ala Glu Arg Ser Tyr His Ile
        275   280   285

10 Phe Tyr Gln Ile Met Ser Asn Lys Lys Pro Asp Leu Ile Glu Met Leu
        290   295   300

Leu Ile Thr Thr Asn Pro Tyr Asp Tyr Ala Phe Val Ser Gln Gly Glu
15 305   310   315   320

Ile Thr Val Pro Ser Ile Asp Asp Gln Glu Glu Leu Met Ala Thr Asp
            325   330   335
20

Ser Ala Ile Glu Ile Leu Gly Phe Thr Ser Asp Glu Arg Val Ser Ile
            340   345   350

25

Tyr Lys Leu Thr Gly Ala Val Met His Tyr Gly Asn Met Lys Phe Lys
        355   360   365

30 Gln Lys Gln Arg Glu Glu Gln Ala Glu Pro Asp Gly Thr Glu Val Ala
        370   375   380

Asp Lys Ala Ala Tyr Leu Gln Asn Leu Asn Ser Ala Asp Leu Leu Lys
35 385   390   395   400

Ala Leu Cys Tyr Pro Arg Val Lys Val Gly Asn Glu Tyr Val Thr Lys
            405   410   415
40

Gly Gln Thr Val Gln Gln Val Tyr Asn Ala Val Gly Ala Leu Ala Lys
        420   425   430

45

Ala Val Tyr Asp Lys Met Phe Leu Trp Met Val Thr Arg Ile Asn Gln
        435   440   445

```
        Gln Leu Asp Thr Lys Gln Pro Arg Gln Tyr Phe Ile Gly Val Leu Asp
            450                 455             460

 5

        Ile Ala Gly Phe Glu Ile Phe Asp Phe Asn Ser Leu Glu Gln Leu Cys
            465             470             475                 480

10      Ile Asn Phe Thr Asn Glu Lys Leu Gln Gln Phe Phe Asn His His Met
                        485             490                 495

        Phe Val Leu Glu Gln Glu Glu Tyr Lys Lys Glu Gly Ile Glu Trp Thr
15                      500             505             510

        Phe Ile Asp Phe Gly Met Asp Leu Ala Ala Cys Ile Glu Leu Ile Glu
                    515             520             525

20

        Lys Pro Met Gly Ile Phe Ser Ile Leu Glu Glu Glu Cys Met Phe Pro
            530             535             540

25

        Lys Ala Thr Asp Thr Ser Phe Lys Asn Lys Leu Tyr Glu Gln His Leu
        545             550             555                 560

30      Gly Lys Ser Asn Asn Phe Gln Lys Pro Lys Pro Ala Lys Gly Lys Pro
                        565             570             575

        Glu Ala His Phe Ser Leu Ile His Tyr Ala Gly Thr Val Asp Tyr Asn
35                  580             585             590

        Ile Ala Gly Trp Leu Asp Lys Asn Lys Asp Pro Leu Asn Glu Thr Val
                595             600             605

40

        Val Gly Leu Tyr Gln Lys Ser Ala Met Lys Thr Leu Ala Leu Leu Phe
            610             615             620

45

        Val Gly Ala Thr Gly Ala Glu Ala Glu Ala Gly Gly Gly Lys Lys Gly
        625             630             635                 640
```

Gly Lys Lys Lys Gly Ser Ser Phe Gln Thr Val Ser Ala Leu Phe Arg
            645   650   655

5

Glu Asn Leu Asn Lys Leu Met Thr Asn Leu Arg Ser Thr His Pro His
         660   665   670

10   Phe Val Arg Cys Ile Ile Pro Asn Glu Thr Lys Thr Pro Gly Ala Met
           675   680   685

Glu His Glu Leu Val Leu His Gln Leu Arg Cys Asn Gly Val Leu Glu
15   690   695   700

Gly Ile Arg Ile Cys Arg Lys Gly Phe Pro Ser Arg Ile Leu Tyr Ala
705   710   715   720
20

Asp Phe Lys Gln Arg Tyr Lys Val Leu Asn Ala Ser Ala Ile Pro Glu
         725   730   735

25

Gly Gln Phe Ile Asp Ser Lys Lys Ala Ser Glu Lys Leu Leu Gly Ser
         740   745   750

30   Ile Asp Ile Asp His Thr Gln Tyr Lys Phe Gly His Thr Lys Val Phe
         755   760   765

Phe Lys Ala Gly Leu Leu Gly Leu Leu Glu Glu Met Arg Asp Glu Lys
35   770   775   780

Leu Ala Gln Leu Ile Thr Arg Thr Gln Ala Met Cys Arg Gly Phe Leu
785   790   795   800
40

Ala Arg Val Glu Tyr Gln Lys Met Val Glu Arg Arg Glu Ser Ile Phe
         805   810   815

45

Cys Ile Gln Tyr Asn Val Arg Ala Phe Met Asn Val Lys His Trp Pro
         820   825   830

Trp Met Lys Leu Tyr Phe Lys Ile Lys Pro Leu Leu Lys Ser Ala Glu
    835   840   845

5

Thr Glu Lys Glu Met Ala Asn Met Lys Glu Glu Phe Glu Lys Thr Lys
    850   855   860

10 Glu Glu Leu Ala Lys Thr Glu Ala Lys Arg Lys Glu Leu Glu Glu Lys
    865   870   875   880

Met Val Thr Leu Met Gln Glu Lys Asn Asp Leu Gln Leu Gln Val Gln
15   885   890   895

Ala Glu Ala Asp Ser Leu Ala Asp Ala Glu Glu Arg Cys Asp Gln Leu
      900   905   910
20

Ile Lys Thr Lys Ile Gln Leu Glu Ala Lys Ile Lys Glu Val Thr Glu
    915   920   925

25

Arg Ala Glu Asp Glu Glu Glu Ile Asn Ala Glu Leu Thr Ala Lys Lys
   930   935   940

30 Arg Lys Leu Glu Asp Glu Cys Ser Glu Leu Lys Lys Asp Ile Asp Asp
  945   950   955   960

Leu Glu Leu Thr Leu Ala Lys Val Glu Lys Glu Lys His Ala Thr Glu
        965   970   975
35

Asn Lys Val Lys Asn Leu Thr Glu Glu Met Ala Gly Leu Asp Glu Thr
     980   985   990
40

Ile Ala Lys Leu Thr Lys Glu Lys Lys Ala Leu Gln Glu Ala His Gln
    995   1000   1005

45

Gln Thr Leu Asp Asp Leu Gln Ala Glu Glu Asp Lys Val Asn Thr
   1010   1015   1020

Leu Thr Lys Ala Lys Ile Lys Leu Glu Gln Gln Val Asp Asp Leu
    1025   1030   1035

5

Glu Gly Ser Leu Glu Gln Glu Lys Lys Ile Arg Met Asp Leu Glu
    1040   1045   1050

10 Arg Ala Lys Arg Lys Leu Glu Gly Asp Leu Lys Leu Ala Gln Glu
        1055   1060   1065

Ser Ala Met Asp Ile Glu Asn Asp Lys Gln Gln Leu Asp Glu Lys
15   1070   1075   ·1080

Leu Lys Lys Lys Glu Phe Glu Met Ser Gly Leu Gln Ser Lys Ile
    ·1085   1090   1095
20

Glu Asp Glu Gln Ala Leu Gly Met Gln Leu Gln Lys Lys Ile Lys
    1100   1105   1110

25

Glu Leu Gln Ala Arg Ile Glu Glu Leu Glu Glu Glu Ile Glu Ala
    1115   1120   1125

30 Glu Arg Ala Ser Arg Ala Lys Ala Glu Lys Gln Arg Ser Asp Leu
        1130   1135   1140

Ser Arg Glu Leu Glu Glu Ile Ser Glu Arg Leu Glu Glu Ala Gly
35   1145   1150   1155

Gly Ala Thr Ser Ala Gln Ile Glu Met Asn Lys Lys Arg Glu Ala
    1160   1165   1170
40

Glu Phe Gln Lys Met Arg Arg Asp Leu Glu Glu Ala Thr Leu Gln
    1175   1180   1185

45

His Glu Ala Thr Ala Ala Thr Leu Arg Lys Lys His Ala Asp Ser
    1190   1195   1200

Val Ala Glu Leu Gly Glu Gln Ile Asp Asn Leu Gln Arg Val Lys
     1205   1210   1215

5

Gln Lys Leu Glu Lys Glu Lys Ser Glu Met Lys Met Glu Ile Asp
     1220   1225   1230

10   Asp Leu Ala Ser Asn Met Glu Thr Val Ser Lys Ala Lys Gly Asn
          1235   1240   1245

Leu Glu Lys Met Cys Arg Ala Leu Glu Asp Gln Leu Ser Glu Ile
15   1250   1255   1260

Lys Thr Lys Glu Glu Glu Gln Gln Arg Leu Ile Asn Asp Leu Thr
     1265   1270   1275
20

Ala Gln Arg Ala Arg Leu Gln Thr Glu Ser Gly Glu Tyr Ser Arg
     1280   1285   1290

25

Gln Leu Asp Glu Lys Asp Thr Leu Val Ser Gln Leu Ser Arg Gly
     1295   1300   1305

30   Lys Gln Ala Phe Thr Gln Gln Ile Glu Glu Leu Lys Arg Gln Leu
          1310   1315   1320

Glu Glu Glu Ile Lys Ala Lys Ser Ala Leu Ala His Ala Leu Gln
35   1325   1330   1335

Ser Ser Arg His Asp Cys Asp Leu Leu Arg Glu Gln Tyr Glu Glu
     1340   1345   1350
40

Glu Gln Glu Ala Lys Ala Glu Leu Gln Arg Ala Met Ser Lys Ala
     1355   1360   1365

45

Asn Ser Glu Val Ala Gln Trp Arg Thr Lys Tyr Glu Thr Asp Ala
     1370   1375   1380

Ile Gln Arg Thr Glu Glu Leu Glu Glu Ala Lys Lys Lys Leu Ala
    1385   1390   1395

5

Gln Arg Leu Gln Asp Ala Glu Glu His Val Glu Ala Val Asn Ala
    1400   1405   1410

10 Lys Cys Ala Ser Leu Glu Lys Thr Lys Gln Arg Leu Gln Asn Glu
        1415   1420   1425

Val Glu Asp Leu Met Ile Asp Val Glu Arg Thr Asn Ala Ala Cys
15   1430   1435   1440

Ala Ala Leu Asp Lys Lys Gln Arg Asn Phe Asp Lys Ile Leu Ala
    1445   1450   1455
20

Glu Trp Lys Gln Lys Cys Glu Glu Thr His Ala Glu Leu Glu Ala
    1460   1465   1470

25

Ser Gln Lys Glu Ser Arg Ser Leu Ser Thr Glu Leu Phe Lys Ile
    1475   1480   1485

30 Lys Asn Ala Tyr Glu Glu Ser Leu Asp Gln Leu Glu Thr Leu Lys
        1490   1495   1500

Arg Glu Asn Lys Asn Leu Gln Gln Glu Ile Ser Asp Leu Thr Glu
35   1505   1510   1515

Gln Ile Ala Glu Gly Gly Lys Arg Ile His Glu Leu Glu Lys Ile
    1520   1525   1530
40

Lys Lys Gln Val Glu Gln Glu Lys Ser Glu Leu Gln Ala Ala Leu
    1535   1540   1545

45

Glu Glu Ala Glu Ala Ser Leu Glu His Glu Glu Gly Lys Ile Leu
    1550   1555   1560

```
Arg Ile  Gln Leu Glu Leu Asn  Gln Val Lys Ser Glu  Val Asp Arg
     1565             1570             1575
```

5

```
Lys Ile  Ala Glu Lys Asp Glu  Glu Ile Asp Gln Met  Lys Arg Asn
     1580             1585             1590
```

10
```
His Ile  Arg Ile Val Glu Ser  Met Gln Ser Thr Leu  Asp Ala Glu
     1595             1600             1605
```

```
Ile Arg  Ser Arg Asn Asp Ala  Ile Arg Leu Lys Lys  Lys Met Glu
```
15
```
     1610             1615             1620
```

```
Gly Asp  Leu Asn Glu Met Glu  Ile Gln Leu Asn His  Ala Asn Arg
     1625             1630             1635
```
20

```
Met Ala  Ala Glu Ala Leu Arg  Asn Tyr Arg Asn Thr  Gln Ala Ile
     1640             1645             1650
```

25
```
Leu Lys  Asp Thr Gln Leu His  Leu Asp Asp Ala Leu  Arg Ser Gln
     1655             1660             1665
```

30
```
Glu Asp  Leu Lys Glu Gln Leu  Ala Met Val Glu Arg  Arg Ala Asn
     1670             1675             1680
```

```
Leu Leu  Gln Ala Glu Ile Glu  Glu Leu Arg Ala Thr  Leu Glu Gln
```
35
```
     1685             1690             1695
```

```
Thr Glu  Arg Ser Arg Lys Ile  Ala Glu Gln Glu Leu  Leu Asp Ala
     1700             1705             1710
```
40

```
Ser Glu  Arg Val Gln Leu Leu  His Thr Gln Asn Thr  Ser Leu Ile
     1715             1720             1725
```

45
```
Asn Thr  Lys Lys Lys Leu Glu  Thr Asp Ile Ser Gln  Ile Gln Gly
     1730             1735             1740
```

```
        Glu Met  Glu Asp Ile Ile Gln  Glu Ala Arg Asn Ala  Glu Glu Lys
           1745                  1750              1755

 5

        Ala Lys  Lys Ala Ile Thr Asp  Ala Ala Met Met Ala  Glu Glu Leu
           1760                  1765              1770

10      Lys Lys  Glu Gln Asp Thr Ser  Ala His Leu Glu Arg  Met Lys Lys
           1775                  1780              1785

        Asn Leu  Glu Gln Thr Val Lys  Asp Leu Gln His Arg  Leu Asp Glu
15         1790                  1795              1800

        Ala Glu  Gln Leu Ala Leu Lys  Gly Gly Lys Lys Gln  Ile Gln Lys
           1805                  1810              1815
20

        Leu Glu  Ala Arg Val Arg Glu  Leu Glu Gly Glu Val  Glu Ser Glu
           1820                  1825              1830

25

        Gln Lys  Arg Asn Val Glu Ala  Val Lys Gly Leu Arg  Lys His Glu
           1835                  1840              1845

30      Arg Lys  Val Lys Glu Leu Thr  Tyr Gln Thr Glu Glu  Asp Arg Lys
           1850                  1855              1860

        Asn Ile  Leu Arg Leu Gln Asp  Leu Val Asp Lys Leu  Gln Ala Lys
35         1865                  1870              1875

        Val Lys  Ser Tyr Lys Arg Gln  Ala Glu Glu Ala Glu  Glu Gln Ser
           1880                  1885              1890
40

        Asn Val  Asn Leu Ser Lys Phe  Arg Arg Ile Gln His  Glu Leu Glu
           1895                  1900              1905

45

        Glu Ala  Glu Glu Arg Ala Asp  Ile Ala Glu Ser Gln  Val Asn Lys
           1910                  1915              1920
```

Leu Arg Val Lys Ser Arg Glu Val His Thr Lys Ile Ile Ser Glu
   1925   1930   1935

5

Glu

10   <210> 7
       <211> 2633
       <212> DNA
       <213> Homo sapiens

15   <220>
       <221> CDS
       <222> (38)..(2584)
       <223>

20   <400> 7
       ccgcggcaag aacatccctc ccagccagca gattaca atg ctg caa act aag gat   55
                                        Met Leu Gln Thr Lys Asp
                                        1   5

25   ctc atc tgg act ttg ttt ttc ctg gga act gca gtt tct ctg cag gtg   103
       Leu Ile Trp Thr Leu Phe Phe Leu Gly Thr Ala Val Ser Leu Gln Val
                  10   15   20

       gat att gtt ccc agc cag ggg gag atc agc gtt gga gag tcc aaa ttc   151
30   Asp Ile Val Pro Ser Gln Gly Glu Ile Ser Val Gly Glu Ser Lys Phe
                  25   30   35

       ttc tta tgc caa gtg gca gga gat gcc aaa gat aaa gac atc tcc tgg   199
       Phe Leu Cys Gln Val Ala Gly Asp Ala Lys Asp Lys Asp Ile Ser Trp
35   40   45   50

       ttc tcc ccc aat gga gaa aag ctc acc cca aac cag cag cgg atc tca   247
       Phe Ser Pro Asn Gly Glu Lys Leu Thr Pro Asn Gln Gln Arg Ile Ser
       55   60   65   70
40

       gtg gtg tgg aat gat gat tcc tcc tcc acc ctc acc atc tat aac gcc   295
       Val Val Trp Asn Asp Asp Ser Ser Ser Thr Leu Thr Ile Tyr Asn Ala
                    75   80   85

45   aac atc gac gac gcc ggc att tac aag tgt gtg gtt aca ggc gag gat   343
       Asn Ile Asp Asp Ala Gly Ile Tyr Lys Cys Val Val Thr Gly Glu Asp
                  90   95   100

```
        ggc agt gag tca gag gcc acc gtc aac gtg aag atc ttt cag aag ctc        391
        Gly Ser Glu Ser Glu Ala Thr Val Asn Val Lys Ile Phe Gln Lys Leu
                105                 110                 115

    5   atg ttc aag aat gcg cca acc cca cag gag ttc cgg gag ggg gaa gat        439
        Met Phe Lys Asn Ala Pro Thr Pro Gln Glu Phe Arg Glu Gly Glu Asp
                120                 125                 130

        gcc gtg att gtg tgt gat gtg gtc agc tcc ctc cca cca acc atc atc        487
   10   Ala Val Ile Val Cys Asp Val Val Ser Ser Leu Pro Pro Thr Ile Ile
        135                 140                 145                 150

        tgg aaa cac aaa ggc cga gat gtc atc ctg aaa aaa gat gtc cga ttc        535
        Trp Lys His Lys Gly Arg Asp Val Ile Leu Lys Lys Asp Val Arg Phe
   15                   155                 160                 165

        ata gtc ctg tcc aac aac tac ctg cag atc cgg ggc atc aag aaa aca        583
        Ile Val Leu Ser Asn Asn Tyr Leu Gln Ile Arg Gly Ile Lys Lys Thr
                        170                 175                 180
   20
        gat gag ggc act tat cgc tgt gag ggc aga atc ctg gca cgg ggg gag        631
        Asp Glu Gly Thr Tyr Arg Cys Glu Gly Arg Ile Leu Ala Arg Gly Glu
                185                 190                 195

   25   atc aac ttc aag gac att cag gtc att gtg aat gtg cca cct acc atc        679
        Ile Asn Phe Lys Asp Ile Gln Val Ile Val Asn Val Pro Pro Thr Ile
                200                 205                 210

        cgg gcc agg cag aat att gtg aat gcc acc gcc aac ctc ggc cag tcc        727
   30   Arg Ala Arg Gln Asn Ile Val Asn Ala Thr Ala Asn Leu Gly Gln Ser
        215                 220                 225                 230

        gtc acc ctg gtg tgc gat gcc gaa cgg ttc cca gag ccc acc atg agc        775
        Val Thr Leu Val Cys Asp Ala Glu Arg Phe Pro Glu Pro Thr Met Ser
   35                   235                 240                 245

        tgg aca aag gat ggg gaa cag ata gag caa gag gaa gac gat gag aag        823
        Trp Thr Lys Asp Gly Glu Gln Ile Glu Gln Glu Glu Asp Asp Glu Lys
                250                 255                 260
   40
        tac atc ttc agc gac gat agt tcc cag ctg acc atc aaa aag gtg gat        871
        Tyr Ile Phe Ser Asp Asp Ser Ser Gln Leu Thr Ile Lys Lys Val Asp
                265                 270                 275

   45   aag aac gac gag gct gag tac atc tgc att gct gag aac aag gct ggc        919
        Lys Asn Asp Glu Ala Glu Tyr Ile Cys Ile Ala Glu Asn Lys Ala Gly
                280                 285                 290
```

gag cag gat gcg acc atc cac ctc aaa gtc ttt gca aaa ccc aaa atc   967
Glu Gln Asp Ala Thr Ile His Leu Lys Val Phe Ala Lys Pro Lys Ile
295   300   305   310

5   aca tat gta gag aac cag act gcc atg gaa tta gag gag cag gtc act   1015
    Thr Tyr Val Glu Asn Gln Thr Ala Met Glu Leu Glu Glu Gln Val Thr
                    315   320   325

    ctt acc tgt gaa gcc tcc gga gac ccc att ccc tcc atc acc tgg agg   1063
10 Leu Thr Cys Glu Ala Ser Gly Asp Pro Ile Pro Ser Ile Thr Trp Arg
                330   335   340

    act tct acc cgg aac atc agc agc gaa gaa aag act ctg gat ggg cac   1111
    Thr Ser Thr Arg Asn Ile Ser Ser Glu Glu Lys Thr Leu Asp Gly His
15   345   350   355

    atg gtg gtg cgt agc cat gcc cgt gtg tcg tcg ctg acc ctg aag agc   1159
    Met Val Val Arg Ser His Ala Arg Val Ser Ser Leu Thr Leu Lys Ser
        360   365   370
20

    atc cag tac act gat gcc gga gag tac atc tgc acc gcc agc aac acc   1207
    Ile Gln Tyr Thr Asp Ala Gly Glu Tyr Ile Cys Thr Ala Ser Asn Thr
    375   380   385   390

25 atc ggc cag gac tcc cag tcc atg tac ctt gaa gtg caa tat gcc cca   1255
    Ile Gly Gln Asp Ser Gln Ser Met Tyr Leu Glu Val Gln Tyr Ala Pro
                    395   400   405

    aag cta cag ggc cct gtg gct gtg tac act tgg gag ggg aac cag gtg   1303
30 Lys Leu Gln Gly Pro Val Ala Val Tyr Thr Trp Glu Gly Asn Gln Val
                    410   415   420

    aac atc acc tgc gag gta ttt gcc tat ccc agt gcc acg atc tca tgg   1351
    Asn Ile Thr Cys Glu Val Phe Ala Tyr Pro Ser Ala Thr Ile Ser Trp
35   425   430   435

    ttt cgg gat ggc cag ctg ctg cca agc tcc aat tac agc aat atc aag   1399
    Phe Arg Asp Gly Gln Leu Leu Pro Ser Ser Asn Tyr Ser Asn Ile Lys
        440   445   450
40

    atc tac aac acc ccc tct gcc agc tat ctg gag gtg acc cca gac tct   1447
    Ile Tyr Asn Thr Pro Ser Ala Ser Tyr Leu Glu Val Thr Pro Asp Ser
    455   460   465   470

45 gag aat gat ttt ggg aac tac aac tgt act gca gtg aac cgc att ggg   1495
    Glu Asn Asp Phe Gly Asn Tyr Asn Cys Thr Ala Val Asn Arg Ile Gly
                475   480   485

```
       cag gag tcc ttc gaa ttc atc ctt gtt caa gca gac acc ccc tct tca      1543
       Gln Glu Ser Phe Glu Phe Ile Leu Val Gln Ala Asp Thr Pro Ser Ser
                   490                 495                 500

   5   cca tcc atc gac cag gtg gag cca tac tcc agc aca gcc cag gtg cag      1591
       Pro Ser Ile Asp Gln Val Glu Pro Tyr Ser Ser Thr Ala Gln Val Gln
                   505                 510                 515

       ttt gat gaa cca gag gcc aca ggt ggg gtg ccc atc ctc aaa tac aaa      1639
  10   Phe Asp Glu Pro Glu Ala Thr Gly Gly Val Pro Ile Leu Lys Tyr Lys
                   520                 525                 530

       gct gag tgg aga gca gtg ggt gaa gaa gta tgg cat tcc aag tgg tat      1687
       Ala Glu Trp Arg Ala Val Gly Glu Glu Val Trp His Ser Lys Trp Tyr
  15   535                 540                 545                 550

       gat gcc aag gaa gcc agc atg gag ggc atc gtc acc atc gtg ggc ctg      1735
       Asp Ala Lys Glu Ala Ser Met Glu Gly Ile Val Thr Ile Val Gly Leu
                       555                 560                 565
  20
       aag ccc gaa aca acg tac gcc gta agg ctg gcg gcg ctc aat ggc aaa      1783
       Lys Pro Glu Thr Thr Tyr Ala Val Arg Leu Ala Ala Leu Asn Gly Lys
                   570                 575                 580

  25   ggg ctg ggt gag atc agc gcg gcc tcc gag ttc aag acg cag cca gtc      1831
       Gly Leu Gly Glu Ile Ser Ala Ala Ser Glu Phe Lys Thr Gln Pro Val
                   585                 590                 595

       caa ggg gaa ccc agt gca cct aag ctc gaa ggg cag atg gga gag gat      1879
  30   Gln Gly Glu Pro Ser Ala Pro Lys Leu Glu Gly Gln Met Gly Glu Asp
                   600                 605                 610

       gga aac tct att aaa gtg aac ctg atc aag cag gat gac ggc ggc tcc      1927
       Gly Asn Ser Ile Lys Val Asn Leu Ile Lys Gln Asp Asp Gly Gly Ser
  35   615                 620                 625                 630

       ccc atc aga cac tat ctg gtc agg tac cga gcg ctc tcc tcc gag tgg      1975
       Pro Ile Arg His Tyr Leu Val Arg Tyr Arg Ala Leu Ser Ser Glu Trp
                       635                 640                 645
  40
       aaa cca gag atc agg ctc ccg tct ggc agt gac cac gtc atg ctg aag      2023
       Lys Pro Glu Ile Arg Leu Pro Ser Gly Ser Asp His Val Met Leu Lys
                   650                 655                 660

  45   tcc ctg gac tgg aat gct gag tat gag gtc tac gtg gtg gct gag aac      2071
       Ser Leu Asp Trp Asn Ala Glu Tyr Glu Val Tyr Val Val Ala Glu Asn
                   665                 670                 675
```

```
     cag caa gga aaa tcc aag gcg gct cat ttt gtg ttc agg acc tcg gcc        2119
     Gln Gln Gly Lys Ser Lys Ala Ala His Phe Val Phe Arg Thr Ser Ala
         680             685             690

 5   cag ccc aca gcc atc cca gcc aac ggc agc ccc acc tca ggc ctg agc        2167
     Gln Pro Thr Ala Ile Pro Ala Asn Gly Ser Pro Thr Ser Gly Leu Ser
     695             700             705             710

     acc ggg gcc atc gtg ggc atc ctc atc gtc atc ttc gtc ctg ctc ctg        2215
10   Thr Gly Ala Ile Val Gly Ile Leu Ile Val Ile Phe Val Leu Leu Leu
                 715             720             725

     gtg gtt gtg gac atc acc tgc tac ttc ctg aac aag tgt ggc ctg ttc        2263
     Val Val Val Asp Ile Thr Cys Tyr Phe Leu Asn Lys Cys Gly Leu Phe
15               730             735             740

     atg tgc att gcg gtc aac ctg tgt gga aaa gcc ggg ccc ggg gcc aag        2311
     Met Cys Ile Ala Val Asn Leu Cys Gly Lys Ala Gly Pro Gly Ala Lys
             745             750             755
20

     ggc aag gac atg gag gag ggc aag gcc gcc ttc tcg aaa gat gag tcc        2359
     Gly Lys Asp Met Glu Glu Gly Lys Ala Ala Phe Ser Lys Asp Glu Ser
         760             765             770

25   aag gag ccc atc gtg gag gtt cga acg gag gag gag agg acc cca aac        2407
     Lys Glu Pro Ile Val Glu Val Arg Thr Glu Glu Glu Arg Thr Pro Asn
     775             780             785             790

     cat gat gga ggg aaa cac aca gag ccc aac gag acc acg cca ctg acg        2455
30   His Asp Gly Gly Lys His Thr Glu Pro Asn Glu Thr Thr Pro Leu Thr
                 795             800             805

     gag ccc gag aag ggc ccc gta gaa gca aag cca gag tgc cag gag aca        2503
     Glu Pro Glu Lys Gly Pro Val Glu Ala Lys Pro Glu Cys Gln Glu Thr
35               810             815             820

     gaa acg aag cca gcg cca gcc gaa gtc aag acg gtc ccc aat gac gcc        2551
     Glu Thr Lys Pro Ala Pro Ala Glu Val Lys Thr Val Pro Asn Asp Ala
             825             830             835
40

     aca cag aca aag gag aac gag agc aaa gca tga tgggtgaaga gaaccgagca      2604
     Thr Gln Thr Lys Glu Asn Glu Ser Lys Ala
         840             845

45   aagatcaaaa taaaaagtga cacagcagc                                       2633


     <210> 8
```

<211> 848
<212> PRT
<213> Homo sapiens

<400> 8

```
Met Leu Gln Thr Lys Asp Leu Ile Trp Thr Leu Phe Phe Leu Gly Thr
1                5                  10               15

Ala Val Ser Leu Gln Val Asp Ile Val Pro Ser Gln Gly Glu Ile Ser
            20                  25               30

Val Gly Glu Ser Lys Phe Phe Leu Cys Gln Val Ala Gly Asp Ala Lys
            35                  40               45

Asp Lys Asp Ile Ser Trp Phe Ser Pro Asn Gly Glu Lys Leu Thr Pro
        50              55                  60

Asn Gln Gln Arg Ile Ser Val Val Trp Asn Asp Asp Ser Ser Ser Thr
65                  70                  75                  80

Leu Thr Ile Tyr Asn Ala Asn Ile Asp Asp Ala Gly Ile Tyr Lys Cys
                85                  90                  95

Val Val Thr Gly Glu Asp Gly Ser Glu Ser Glu Ala Thr Val Asn Val
                100                 105                 110

Lys Ile Phe Gln Lys Leu Met Phe Lys Asn Ala Pro Thr Pro Gln Glu
            115                 120                 125

Phe Arg Glu Gly Glu Asp Ala Val Ile Val Cys Asp Val Val Ser Ser
        130                 135                 140

Leu Pro Pro Thr Ile Ile Trp Lys His Lys Gly Arg Asp Val Ile Leu
145                 150                 155                 160

Lys Lys Asp Val Arg Phe Ile Val Leu Ser Asn Asn Tyr Leu Gln Ile
                165                 170                 175
```

Arg Gly Ile Lys Lys Thr Asp Glu Gly Thr Tyr Arg Cys Glu Gly Arg
            180   185   190

Ile Leu Ala Arg Gly Glu Ile Asn Phe Lys Asp Ile Gln Val Ile Val
            195   200   205

Asn Val Pro Pro Thr Ile Arg Ala Arg Gln Asn Ile Val Asn Ala Thr
            210   215   220

Ala Asn Leu Gly Gln Ser Val Thr Leu Val Cys Asp Ala Glu Arg Phe
225   230   235   240

Pro Glu Pro Thr Met Ser Trp Thr Lys Asp Gly Glu Gln Ile Glu Gln
                    245   250   255

Glu Glu Asp Asp Glu Lys Tyr Ile Phe Ser Asp Asp Ser Ser Gln Leu
            260   265   270

Thr Ile Lys Lys Val Asp Lys Asn Asp Glu Ala Glu Tyr Ile Cys Ile
            275   280   285

Ala Glu Asn Lys Ala Gly Glu Gln Asp Ala Thr Ile His Leu Lys Val
            290   295   300

Phe Ala Lys Pro Lys Ile Thr Tyr Val Glu Asn Gln Thr Ala Met Glu
305   310   315   320

Leu Glu Glu Gln Val Thr Leu Thr Cys Glu Ala Ser Gly Asp Pro Ile
                    325   330   335

Pro Ser Ile Thr Trp Arg Thr Ser Thr Arg Asn Ile Ser Ser Glu Glu
            340   345   350

Lys Thr Leu Asp Gly His Met Val Val Arg Ser His Ala Arg Val Ser
            355   360   365

Ser Leu Thr Leu Lys Ser Ile Gln Tyr Thr Asp Ala Gly Glu Tyr Ile
370   375   380

Cys Thr Ala Ser Asn Thr Ile Gly Gln Asp Ser Gln Ser Met Tyr Leu
385   390   395   400

Glu Val Gln Tyr Ala Pro Lys Leu Gln Gly Pro Val Ala Val Tyr Thr
405   410   415

Trp Glu Gly Asn Gln Val Asn Ile Thr Cys Glu Val Phe Ala Tyr Pro
420   425   430

Ser Ala Thr Ile Ser Trp Phe Arg Asp Gly Gln Leu Leu Pro Ser Ser
435   440   445

Asn Tyr Ser Asn Ile Lys Ile Tyr Asn Thr Pro Ser Ala Ser Tyr Leu
450   455   460

Glu Val Thr Pro Asp Ser Glu Asn Asp Phe Gly Asn Tyr Asn Cys Thr
465   470   475   480

Ala Val Asn Arg Ile Gly Gln Glu Ser Phe Glu Phe Ile Leu Val Gln
485   490   495

Ala Asp Thr Pro Ser Ser Pro Ser Ile Asp Gln Val Glu Pro Tyr Ser
500   505   510

Ser Thr Ala Gln Val Gln Phe Asp Glu Pro Glu Ala Thr Gly Gly Val
515   520   525

Pro Ile Leu Lys Tyr Lys Ala Glu Trp Arg Ala Val Gly Glu Glu Val
530   535   540

Trp His Ser Lys Trp Tyr Asp Ala Lys Glu Ala Ser Met Glu Gly Ile
545   550   555   560

Val Thr Ile Val Gly Leu Lys Pro Glu Thr Thr Tyr Ala Val Arg Leu
          565   570   575

5

Ala Ala Leu Asn Gly Lys Gly Leu Gly Glu Ile Ser Ala Ala Ser Glu
          580   585   590

10

Phe Lys Thr Gln Pro Val Gln Gly Glu Pro Ser Ala Pro Lys Leu Glu
          595   600   605

15   Gly Gln Met Gly Glu Asp Gly Asn Ser Ile Lys Val Asn Leu Ile Lys
          610   615   620

Gln Asp Asp Gly Gly Ser Pro Ile Arg His Tyr Leu Val Arg Tyr Arg
20 625   630   635   640

Ala Leu Ser Ser Glu Trp Lys Pro Glu Ile Arg Leu Pro Ser Gly Ser
          645   650   655

25

Asp His Val Met Leu Lys Ser Leu Asp Trp Asn Ala Glu Tyr Glu Val
          660   665   670

30·

Tyr Val Val Ala Glu Asn Gln Gln Gly Lys Ser Lys Ala Ala His Phe
          675   680   685

35   Val Phe Arg Thr Ser Ala Gln Pro Thr Ala Ile Pro Ala Asn Gly Ser
          690   695   700

Pro Thr Ser Gly Leu Ser Thr Gly Ala Ile Val Gly Ile Leu Ile Val
40 705   710   715   720

Ile Phe Val Leu Leu Leu Val Val Val Asp Ile Thr Cys Tyr Phe Leu
          725   730   735

45

Asn Lys Cys Gly Leu Phe Met Cys Ile Ala Val Asn Leu Cys Gly Lys
          740   745   750

Ala Gly Pro Gly Ala Lys Gly Lys Asp Met Glu Glu Gly Lys Ala Ala
        755   760   765

Phe Ser Lys Asp Glu Ser Lys Glu Pro Ile Val Glu Val Arg Thr Glu
        770   775   780

Glu Glu Arg Thr Pro Asn His Asp Gly Gly Lys His Thr Glu Pro Asn
785   790   795   800

Glu Thr Thr Pro Leu Thr Glu Pro Glu Lys Gly Pro Val Glu Ala Lys
                 805   810   815

Pro Glu Cys Gln Glu Thr Glu Thr Lys Pro Ala Pro Ala Glu Val Lys
             820   825   830

Thr Val Pro Asn Asp Ala Thr Gln Thr Lys Glu Asn Glu Ser Lys Ala
             835   840   845

<210> 9
<211> 1692
<212> DNA
<213> Homo sapiens;

<220>
<221> CDS
<222> (121)..(1080)
<223>

<300>
<308> X56677
<309> 1991-03-19
<313> (1)..(1692)

<400> 9
attcagactg ccagcacttt gctatctaca gccggggctc ccgagcggca gaaagttccg   60

gccactctct gccgcttggg ttgggcgaaa gccaggaccg tgccgcgcca ccgccaggat   120

atg gag cta ctg tcg cca ccg ctc cgc gac gta gac ctg acg gcc ccc   168
Met Glu Leu Leu Ser Pro Pro Leu Arg Asp Val Asp Leu Thr Ala Pro

```
           1                    5                         10                        15

      gac ggc tct ctc tgc tcc ttt gcc aca acg gac gac ttc tat gac gac    216
      Asp Gly Ser Leu Cys Ser Phe Ala Thr Thr Asp Asp Phe Tyr Asp Asp
 5                20                      25                      30

      ccg tgt ttc gac tcc ccg gac ctg cgc ttc ttc gaa gac ctg gac ccg    264
      Pro Cys Phe Asp Ser Pro Asp Leu Arg Phe Phe Glu Asp Leu Asp Pro
                  35                      40                      45
10
      cgc ctg atg cac gtg ggc gcg ctc ctg aaa ccc gaa gag cac tcg cac    312
      Arg Leu Met His Val Gly Ala Leu Leu Lys Pro Glu Glu His Ser His
                  50                      55                      60

15    ttc ccc gcg gcg gtg cac ccg gcc ccg ggc gca cgt gag gac gag cat    360
      Phe Pro Ala Ala Val His Pro Ala Pro Gly Ala Arg Glu Asp Glu His
      65                      70                      75                      80

      gtg cgc gcg ccc agc ggg cac cac cag gcg ggc cgc tgc cta ctg tgg    408
20    Val Arg Ala Pro Ser Gly His His Gln Ala Gly Arg Cys Leu Leu Trp
                          85                      90                      95

      gcc tgc aag gcg tgc aag cgc aag acc acc aac gcc gac cgc cgc aag    456
      Ala Cys Lys Ala Cys Lys Arg Lys Thr Thr Asn Ala Asp Arg Arg Lys
25                        100                     105                     110

      gcc gcc acc atg cgc gag cgg cgc cgc ctg agc aaa gta aat gag gcc    504
      Ala Ala Thr Met Arg Glu Arg Arg Arg Leu Ser Lys Val Asn Glu Ala
                      115                     120                     125
30
      ttt gag aca ctc aag cgc tgc acg tcg agc aat cca aac cag cgg ttg    552
      Phe Glu Thr Leu Lys Arg Cys Thr Ser Ser Asn Pro Asn Gln Arg Leu
                  130                     135                     140

35    ccc aag gtg gag atc ctg cgc aac gcc atc cgc tat atc gag ggc ctg    600
      Pro Lys Val Glu Ile Leu Arg Asn Ala Ile Arg Tyr Ile Glu Gly Leu
      145                     150                     155                     160

      cag gct ctg ctg cgc gac cag gac gcc gcg ccc cct ggc gca gcc gcc    648
40    Gln Ala Leu Leu Arg Asp Gln Asp Ala Ala Pro Pro Gly Ala Ala Ala
                      165                     170                     175

      ttc tat gcg ccg ggc ccg ctg ccc ccg ggc cgc ggc ggc gag cac tac    696
      Phe Tyr Ala Pro Gly Pro Leu Pro Pro Gly Arg Gly Gly Glu His Tyr
45                    180                     185                     190

      agc ggc gac tcc gac gcg tcc agc ccg cgc tcc aac tgc tcc gac ggc    744
      Ser Gly Asp Ser Asp Ala Ser Ser Pro Arg Ser Asn Cys Ser Asp Gly
```

```
            195                 200                 205

    atg atg gac tac agc ggc ccc ccg agc ggc gcc cgg cgg cgg aac tgc     792
    Met Met Asp Tyr Ser Gly Pro Pro Ser Gly Ala Arg Arg Arg Asn Cys
 5      210                 215                 220

    tac gaa ggc gcc tac tac aac gag gcg ccc agc gaa ccc agg ccc ggg     840
    Tyr Glu Gly Ala Tyr Tyr Asn Glu Ala Pro Ser Glu Pro Arg Pro Gly
    225                 230                 235                 240
10

    aag agt gcg gcg gtg tcg agc cta gac tac ctg tcc agc atc gtg gag     888
    Lys Ser Ala Ala Val Ser Ser Leu Asp Tyr Leu Ser Ser Ile Val Glu
                        245                 250                 255

15  cgc atc tcc acc gag agc cct gcg gcg ccc gcc ctc ctg ctg gcg gac     936
    Arg Ile Ser Thr Glu Ser Pro Ala Ala Pro Ala Leu Leu Leu Ala Asp
                    260                 265                 270

    gtg cct tct gag tcg cct ccg cgc agg caa gag gct gcc gcc ccc agc     984
20  Val Pro Ser Glu Ser Pro Pro Arg Arg Gln Glu Ala Ala Ala Pro Ser
                275                 280                 285

    gag gga gag agc agc ggc gac ccc acc cag tca ccg gac gcc gcc ccg    1032
    Glu Gly Glu Ser Ser Gly Asp Pro Thr Gln Ser Pro Asp Ala Ala Pro
25      290                 295                 300

    cag tgc cct gcg ggt gcg aac ccc aac ccg ata tac cag gtg ctc tga    1080
    Gln Cys Pro Ala Gly Ala Asn Pro Asn Pro Ile Tyr Gln Val Leu
    305                 310                 315
30
    gggggatgtg gccgcccaac cccgccaggg atggtgccct agggtccctc gcgcccaaaa   1140

    gattgaactt aaatgccccc ctcccaacag cgctttaaaa gcgccatctc ttgaggtagg   1200

35  agaggcggag aactgaagtt tccgcccccc ccgacagggc aaggacacag cgcggttttt   1260

    tccacgcagc acccttctcg agacccatt gcgatggccg ctccgtgttc ctcggtgggc    1320

    cagagctgaa ccttgagggg ctaggttcac gtttctcgcg ccctccatgg tgagaccctc   1380
40
    gcagacctaa ccctgccccg ggatgcaccg gttatttggg ggggcgtgag acagtgcact   1440

    ccggtcccaa atgtagcagg tgtaaccgta acccaccccc aacccgtttc ccggttcagg   1500

45  accacttttt gtaatacttt ttgtaatcta ttcctgtaaa taagagttcg tttgccagag   1560

    aggagcccct ggggctgtat ttatctctga ggcagggtgt gtggtgctac agggaatttg   1620
```

```
tacgtttata ccgcaggcgg gcgagccgcg ggcgctcgct caggtgatca aaataaaggc   1680

gctaatttat aa                                                       1692
```

<210> 10
<211> 319
<212> PRT
<213> Homo sapiens;

<400> 10

```
Met Glu Leu Leu Ser Pro Pro Leu Arg Asp Val Asp Leu Thr Ala Pro
1               5                   10                  15


Asp Gly Ser Leu Cys Ser Phe Ala Thr Thr Asp Asp Phe Tyr Asp Asp
            20                  25                  30


Pro Cys Phe Asp Ser Pro Asp Leu Arg Phe Phe Glu Asp Leu Asp Pro
            35                  40                  45


Arg Leu Met His Val Gly Ala Leu Leu Lys Pro Glu Glu His Ser His
    50                  55                  60


Phe Pro Ala Ala Val His Pro Ala Pro Gly Ala Arg Glu Asp Glu His
65                  70                  75                  80


Val Arg Ala Pro Ser Gly His His Gln Ala Gly Arg Cys Leu Leu Trp
                85                  90                  95


Ala Cys Lys Ala Cys Lys Arg Lys Thr Thr Asn Ala Asp Arg Arg Lys
                100                 105                 110


Ala Ala Thr Met Arg Glu Arg Arg Arg Leu Ser Lys Val Asn Glu Ala
            115                 120                 125


Phe Glu Thr Leu Lys Arg Cys Thr Ser Ser Asn Pro Asn Gln Arg Leu
            130                 135                 140
```

Pro Lys Val Glu Ile Leu Arg Asn Ala Ile Arg Tyr Ile Glu Gly Leu
145   150   155   160

5   Gln Ala Leu Leu Arg Asp Gln Asp Ala Ala Pro Pro Gly Ala Ala Ala
                        165   170   175

10 Phe Tyr Ala Pro Gly Pro Leu Pro Pro Gly Arg Gly Gly Glu His Tyr
                        180   185   190

15 Ser Gly Asp Ser Asp Ala Ser Ser Pro Arg Ser Asn Cys Ser Asp Gly
                        195   200   205

    Met Met Asp Tyr Ser Gly Pro Pro Ser Gly Ala Arg Arg Arg Asn Cys
                        210   215   220

20

    Tyr Glu Gly Ala Tyr Tyr Asn Glu Ala Pro Ser Glu Pro Arg Pro Gly
    225   230   235   240

25 Lys Ser Ala Ala Val Ser Ser Leu Asp Tyr Leu Ser Ser Ile Val Glu
                        245   250   255

30 Arg Ile Ser Thr Glu Ser Pro Ala Ala Pro Ala Leu Leu Leu Ala Asp
                        260   265   270

35 Val Pro Ser Glu Ser Pro Pro Arg Arg Gln Glu Ala Ala Ala Pro Ser
                        275   280   285

    Glu Gly Glu Ser Ser Gly Asp Pro Thr Gln Ser Pro Asp Ala Ala Pro
        290   295   300

40

    Gln Cys Pro Ala Gly Ala Asn Pro Asn Pro Ile Tyr Gln Val Leu
    305   310   315

45 <210> 11
    <211> 1427
    <212> DNA
    <213> Homo sapiens;

<220>
<221> CDS
<222> (43)..(810)
<223>

<300>
<308> NM_005593
<309> 2003-04-07
<313> (1)..(1427)

<400> 11
cctctcgctg ccgtccaggt gcaccgcctg cctctcagca gg atg gac gtg atg   54
                                                Met Asp Val Met
                                                1

gat ggc tgc cag ttc tca cct tct gag tac ttc tac gac ggc tcc tgc   102
Asp Gly Cys Gln Phe Ser Pro Ser Glu Tyr Phe Tyr Asp Gly Ser Cys
5   10   15   20

ata ccg tcc ccc gag ggt gaa ttt ggg gac gag ttt gtg ccg cga gtg   150
Ile Pro Ser Pro Glu Gly Glu Phe Gly Asp Glu Phe Val Pro Arg Val
                25   30   35

gct gcc ttc gga gcg cac aaa gca gag ctg cag ggc tca gat gag gac   198
Ala Ala Phe Gly Ala His Lys Ala Glu Leu Gln Gly Ser Asp Glu Asp
                40   45   50

gag cac gtg cga gcg cct acc ggc cac cac cag gct ggt cac tgc ctc   246
Glu His Val Arg Ala Pro Thr Gly His His Gln Ala Gly His Cys Leu
                55   60   65

atg tgg gcc tgc aaa gcc tgc aag agg aag tcc acc acc atg gat cgg   294
Met Trp Ala Cys Lys Ala Cys Lys Arg Lys Ser Thr Thr Met Asp Arg
        70   75   80

cgg aag gca gcc act atg cgc gag cgg agg cgc ctg aag aag gtc aac   342
Arg Lys Ala Ala Thr Met Arg Glu Arg Arg Arg Leu Lys Lys Val Asn
85   90   95   100

cag gct ttc gaa acc ctc aag agg tgt acc acg acc aac ccc aac cag   390
Gln Ala Phe Glu Thr Leu Lys Arg Cys Thr Thr Thr Asn Pro Asn Gln
                105   110   115

agg ctg ccc aag gtg gag atc ctc agg aat gcc atc cgc tac atc gag   438
Arg Leu Pro Lys Val Glu Ile Leu Arg Asn Ala Ile Arg Tyr Ile Glu
                120   125   130

```
   agc ctg cag gag ttg ctg aga gag cag gtg gag aac tac tat agc ctg        486
   Ser Leu Gln Glu Leu Leu Arg Glu Gln Val Glu Asn Tyr Tyr Ser Leu
           135                 140                 145

5  ccg gga cag agc tgc tcg gag ccc acc agc ccc acc tcc aac tgc tct        534
   Pro Gly Gln Ser Cys Ser Glu Pro Thr Ser Pro Thr Ser Asn Cys Ser
           150                 155                 160

   gat ggc atg ccc gaa tgt aac agt cct gtc tgg tcc aga aag agc agt        582
10 Asp Gly Met Pro Glu Cys Asn Ser Pro Val Trp Ser Arg Lys Ser Ser
   165                 170                 175                 180

   act ttt gac agc atc tac tgt cct gat gta tca aat gta tat gcc aca        630
   Thr Phe Asp Ser Ile Tyr Cys Pro Asp Val Ser Asn Val Tyr Ala Thr
15                 185                 190                 195

   gat aaa aac tcc tta tcc agc ttg gat tgc tta tcc aac ata gtg gac        678
   Asp Lys Asn Ser Leu Ser Ser Leu Asp Cys Leu Ser Asn Ile Val Asp
                   200                 205                 210
20
   cgg atc acc tcc tca gag caa cct ggg ttg cct ctc cag gat ctg gct        726
   Arg Ile Thr Ser Ser Glu Gln Pro Gly Leu Pro Leu Gln Asp Leu Ala
                   215                 220                 225

25 tct ctc tct cca gtt gcc agc acc gat tca cag cct cga act cca ggg        774
   Ser Leu Ser Pro Val Ala Ser Thr Asp Ser Gln Pro Arg Thr Pro Gly
           230                 235                 240

   gct tct agt tcc agg ctt atc tat cat gtg cta tga actaattttc            820
30 Ala Ser Ser Ser Arg Leu Ile Tyr His Val Leu
   245                 250                 255

 , tggtctatat gacttcttcc aggagggcct aatacacagg acgaagaagg cttcaaaaag    880

35 tcccaaacca agacaacatg tacataaaga tttctttca gttgtaaatt tgtaaagatt      940

   accttgccac tttataagaa agtgtattta actaaaaagt catcattgca aataatactt    1000

   tcttcttctt tattattctt tgcttagata ttaatacata gttccagtaa tactatttct    1060
40
   gataggggc cattgattga gggtagcttg ttcgaatgct taacttatat atacatatat    1120

   atatattata aatattgctc atcaaaatgt ctctggtgtt tagagcttta ttttttctt    1180

45 taaaacatta aaacagctga gaatcagtta aatggaattt taaatatatt taactatttc    1240

   ttttctcttt aatcctttag ttatattgta ttaaataaaa atataatact gcctaatgta    1300
```

tatattttga tcttttcttg taagaaatgt atctttttaaa tgtaagcaca aaatagtact   1360

ttgtggatca tttcaagata taagaaattt tggaaattcc accataaata aaatttttta   1420

ctacaag   1427

<210> 12
<211> 255
<212> PRT
<213> Homo sapiens;

<400> 12

Met Asp Val Met Asp Gly Cys Gln Phe Ser Pro Ser Glu Tyr Phe Tyr
1   5   10   15

Asp Gly Ser Cys Ile Pro Ser Pro Glu Gly Glu Phe Gly Asp Glu Phe
            20   25   30

Val Pro Arg Val Ala Ala Phe Gly Ala His Lys Ala Glu Leu Gln Gly
            35   40   45

Ser Asp Glu Asp Glu His Val Arg Ala Pro Thr Gly His His Gln Ala
            50   55   60

Gly His Cys Leu Met Trp Ala Cys Lys Ala Cys Lys Arg Lys Ser Thr
65   70   75   80

Thr Met Asp Arg Arg Lys Ala Ala Thr Met Arg Glu Arg Arg Arg Leu
                85   90   95

Lys Lys Val Asn Gln Ala Phe Glu Thr Leu Lys Arg Cys Thr Thr Thr
            100   105   110

Asn Pro Asn Gln Arg Leu Pro Lys Val Glu Ile Leu Arg Asn Ala Ile
            115   120   125

Arg Tyr Ile Glu Ser Leu Gln Glu Leu Leu Arg Glu Gln Val Glu Asn
            130   135   140

Tyr Tyr Ser Leu Pro Gly Gln Ser Cys Ser Glu Pro Thr Ser Pro Thr
145   150   155   160

Ser Asn Cys Ser Asp Gly Met Pro Glu Cys Asn Ser Pro Val Trp Ser
165   170   175

Arg Lys Ser Ser Thr Phe Asp Ser Ile Tyr Cys Pro Asp Val Ser Asn
180   185   190

Val Tyr Ala Thr Asp Lys Asn Ser Leu Ser Ser Leu Asp Cys Leu Ser
195   200   205

Asn Ile Val Asp Arg Ile Thr Ser Ser Glu Gln Pro Gly Leu Pro Leu
210   215   220

Gln Asp Leu Ala Ser Leu Ser Pro Val Ala Ser Thr Asp Ser Gln Pro
225   230   235   240

Arg Thr Pro Gly Ala Ser Ser Ser Arg Leu Ile Tyr His Val Leu
245   250   255

<210> 13
<211> 675
<212> DNA
<213> Homo sapiens:

<220>
<221> CDS
<222> (1)..(675)
<223>

<300>
<308> BT007233
<309> 2003-05-13
<313> (1)..(675)

<400> 13

atg gag ctg tat gag aca tcc ccc tac ttc tac cag gaa ccc cgc ttc   48
Met Glu Leu Tyr Glu Thr Ser Pro Tyr Phe Tyr Gln Glu Pro Arg Phe

```
              1               5                    10                      15

         tat gat ggg gaa aac tac ctg cct gtc cac ctc cag ggc ttc gaa cca       96
         Tyr Asp Gly Glu Asn Tyr Leu Pro Val His Leu Gln Gly Phe Glu Pro
    5                  20                  25                  30

         cca ggc tac gag cgg acg gag ctc acc ctg agc ccc gag gcc cca ggg      144
         Pro Gly Tyr Glu Arg Thr Glu Leu Thr Leu Ser Pro Glu Ala Pro Gly
                       35                  40                  45
   10
         ccc ctt gag gac aag ggg ctg ggg acc ccc gag cac tgt cca ggc cag      192
         Pro Leu Glu Asp Lys Gly Leu Gly Thr Pro Glu His Cys Pro Gly Gln
                    50                  55                  60

   15    tgc ctg ccg tgg gcg tgt aag gtg tgt aag agg aag tcg gtg tcc gtg      240
         Cys Leu Pro Trp Ala Cys Lys Val Cys Lys Arg Lys Ser Val Ser Val
         65                  70                  75                  80

         gac cgg cgg cgg gcg gcc aca ctg agg gag aag cgc agg ctc aag aag      288
   20    Asp Arg Arg Arg Ala Ala Thr Leu Arg Glu Lys Arg Arg Leu Lys Lys
                       85                  90                  95

         gtg aat gag gcc ttc gag gcc ctg aag aga agc acc ctg ctc aac ccc      336
         Val Asn Glu Ala Phe Glu Ala Leu Lys Arg Ser Thr Leu Leu Asn Pro
   25                 100                 105                 110

         aac cag cgg ctg ccc aag gtg gag atc ctg cgc agt gcc atc cag tac      384
         Asn Gln Arg Leu Pro Lys Val Glu Ile Leu Arg Ser Ala Ile Gln Tyr
                      115                 120                 125
   30
         atc gag cgc ctc cag gcc ctg ctc agc tcc ctc aac cag gag gag cgt      432
         Ile Glu Arg Leu Gln Ala Leu Leu Ser Ser Leu Asn Gln Glu Glu Arg
                    130                 135                 140

   35    gac ctc cgc tac cgg ggc ggg ggc ggg ccc cag cca ggg gtg ccc agc      480
         Asp Leu Arg Tyr Arg Gly Gly Gly Gly Pro Gln Pro Gly Val Pro Ser
         145                 150                 155                 160

         gaa tgc agc tct cac agc gcc tcc tgc agt cca gag tgg ggc agt gca      528
   40    Glu Cys Ser Ser His Ser Ala Ser Cys Ser Pro Glu Trp Gly Ser Ala
                      165                 170                 175

         ctg gag ttc agc gcc aac cca ggg gat cat ctg ctc acg gct gac cct      576
         Leu Glu Phe Ser Ala Asn Pro Gly Asp His Leu Leu Thr Ala Asp Pro
   45                 180                 185                 190

         aca gat gcc cac aac ctg cac tcc ctc acc tcc atc gtg gac agc atc      624
         Thr Asp Ala His Asn Leu His Ser Leu Thr Ser Ile Val Asp Ser Ile
```

```
             195              200                205

     aca gtg gaa gat gtg tct gtg gcc ttc cca gat gaa acc atg ccc aac    672
     Thr Val Glu Asp Val Ser Val Ala Phe Pro Asp Glu Thr Met Pro Asn
 5   210              215                220

     tag                                                                675
```

10 <210> 14
    <211> 224
    <212> PRT
    <213> Homo sapiens;

15 <400> 14

```
    Met Glu Leu Tyr Glu Thr Ser Pro Tyr Phe Tyr Gln Glu Pro Arg Phe
    1                   5                   10                  15
```

20

```
    Tyr Asp Gly Glu Asn Tyr Leu Pro Val His Leu Gln Gly Phe Glu Pro
                20                  25                  30
```

25

```
    Pro Gly Tyr Glu Arg Thr Glu Leu Thr Leu Ser Pro Glu Ala Pro Gly
                35                  40                  45
```

```
    Pro Leu Glu Asp Lys Gly Leu Gly Thr Pro Glu His Cys Pro Gly Gln
30      50                  55                  60
```

```
    Cys Leu Pro Trp Ala Cys Lys Val Cys Lys Arg Lys Ser Val Ser Val
    65                  70                  75                  80
35
```

```
    Asp Arg Arg Arg Ala Ala Thr Leu Arg Glu Lys Arg Arg Leu Lys Lys
                85                  90                  95
```

40

```
    Val Asn Glu Ala Phe Glu Ala Leu Lys Arg Ser Thr Leu Leu Asn Pro
                100                 105                 110
```

```
45  Asn Gln Arg Leu Pro Lys Val Glu Ile Leu Arg Ser Ala Ile Gln Tyr
                115                 120                 125
```

Ile Glu Arg Leu Gln Ala Leu Leu Ser Ser Leu Asn Gln Glu Glu Arg
     130   135   140

Asp Leu Arg Tyr Arg Gly Gly Gly Gly Pro Gln Pro Gly Val Pro Ser
     145   150   155   160

Glu Cys Ser Ser His Ser Ala Ser Cys Ser Pro Glu Trp Gly Ser Ala
              165   170   175

Leu Glu Phe Ser Ala Asn Pro Gly Asp His Leu Leu Thr Ala Asp Pro
         180   185   190

Thr Asp Ala His Asn Leu His Ser Leu Thr Ser Ile Val Asp Ser Ile
       195   200   205

Thr Val Glu Asp Val Ser Val Ala Phe Pro Asp Glu Thr Met Pro Asn
     210   215   220

<210> 15
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> SRY forward primer

<400> 15
gcctcaggac atattaatct ctggag   26

<210> 16
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> SRY reverse primer

<400> 16
gctgatctct gaattctgca tgc   23

<210> 17
<211> 26
<212> DNA
<213> Artificial Sequence

5

<220>
<223> SRY probe

<400> 17
10 aggcgcaagt tggctcaaca gaatcc   26

<210> 18
<211> 25
15 <212> DNA
<213> Artificial Sequence

<220>
<223> IL2 forward primer

20
<400> 18
gccttgtgtg ttataagtag gaggc   25

25 <210> 19
<211> 21
<212> DNA
<213> Artificial Sequence

30 <220>
<223> IL2 reverse primer

<400> 19
agtgccaatt cgatgatgag c   21
35

<210> 20
<211> 29
<212> DNA
40 <213> Artificial Sequence

<220>
<223> IL2 probe

45 <400> 20
tctcctcaga aattccacca cagttgctg   29